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OM protein - protein search, using sw model

Run on: November 8, 2005, 20:40:37 ; Search time 165 Seconds
(without alignments)
447.704 Million cell updates/sec

Title: US-09-805-354-1
Sequence: 1 CPQEDSDIAFLIDSGSIIP.....VNFEALKTIONQREKKFA 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	974	99.8	194	8	ADR23221 Human int
2	974	99.8	1152	8	ADM9589 Human int
3	974	99.8	1152	8	ADP12435 Protein e
4	974	99.8	1153	2	AAR04136 Alpha sub
5	974	99.8	1153	2	AAW65090 Human Bet
6	974	99.8	1153	3	AAU807360 Human CDI
7	974	99.8	1153	5	ABG61469 Human int
8	974	99.8	1153	5	ABG61469 Human Bet
9	974	99.8	1153	7	AAO14428 Integrin
10	974	99.8	1153	7	ADD25615 Binding d
11	974	99.8	1153	8	ADR23250 Human int
12	974	99.8	1153	8	ADR23250 Human int
13	974	99.8	1153	8	ADR23250 Human int
14	974	99.8	1153	8	ADR23250 Human int
15	974	99.8	1153	8	ADR23250 Human int
16	974	99.8	1153	8	ADR23250 Human int
17	974	99.8	1153	8	ADR23250 Human int
18	974	99.8	1153	8	ADR23250 Human int
19	974	99.8	1153	8	ADR23250 Human int
20	974	99.8	1153	8	ADR23250 Human int
21	974	99.8	1153	8	ADR23250 Human int
22	974	99.8	1153	8	ADR23250 Human int
23	974	99.8	1153	8	ADR23250 Human int
24	974	99.8	1153	8	ADR23250 Human int
25	974	99.8	1153	8	ADR23250 Human int

26	603	61.8	1151	5	ABG61480	ABG61480 Rat Betaz
27	603	61.8	1161	2	AAR78169	Aar78169 Rat alpha
28	603	61.8	1161	2	AAW23062	Aaw23062 Rat beta
29	603	61.8	1161	2	AAW60004	Aaw60004 Rat alpha
30	603	61.8	1161	2	AAW65104	Aaw65104 Rat beta
31	603	61.8	1161	2	AAW72824	Aaw72824 Rat alpha
32	603	61.8	1161	2	AAW73345	Aaw73345 Rat alpha
33	603	61.8	1161	3	AAW73374	AAW73374 Rat alpha
34	603	61.8	1161	5	ABG61483	ABG61483 Rat Betaz
35	602	61.7	413	2	AAW23065	AAW23065 Rabbit de
36	602	61.7	413	2	AAW65107	AAW65107 Rabbit de
37	602	61.7	413	2	AAW72839	AAW72839 Rabbit al
38	602	61.7	413	2	AAW73348	AAW73348 Rabbit al
39	602	61.7	413	3	AAW73377	AAW73377 Rabbit al
40	602	61.7	1151	2	AAW78179	AAW78179 Rat alpha
41	600	61.5	1151	5	ABG61486	ABG61486 Rabbit Be
42	594	60.9	1155	2	AAR78167	Aar78167 Mouse bet
43	594	60.9	1155	2	AAW23060	AAW23060 Mouse bet
44	594	60.9	1155	2	AAW60002	AAW60002 Mouse alp
45	594	60.9	1155	2	AAW65102	AAW65102 Mouse bet

ALIGNMENTS

RESULT 1
ADR23221 standard; protein; 194 AA.

AC ADR23221;

DT 04-NOV-2004 (first entry)

DE Human integrin CD11b alpha subunit A domain.

KW Human; integrin; CD11b; inflammation; antiinflammatory; vasotropic.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 1..191

FT Misc-difference 189 /label = A_domain

FT /note= "Invariant Ile residue"

PN WO2004066914-A2.

PD 12-AUG-2004.

PF 12-MAY-2003; 2003WO-US014919.

PR 10-MAY-2002; 2002US-00144259.

PA (GENO) GEN HOSPITAL CORP.

PI Arnaout MA, Li R, Xiong J;

DR MPI; 2004-593980/57.

PT Novel variant integrin CD11b alpha subunit polypeptide, useful for

PT determining candidate compound for binding to CD11b, and for determining

PT compound as activation-dependent ligand.

PS Disclosure; SEQ ID NO 1; 128pp; English.

XX The present sequence is that of the human integrin alpha subunit CD11b A
XX domain. This includes an invariant Ile residue. The invention features
XX variant integrin alpha subunit polypeptides in which the invariant Ile is
XX substituted by Gly, Ala or some other amino acid (e.g. Val) or is
XX deleted. The polypeptide can include part or all of the A domain.
XX Replacing the invariant Ile creates a variant integrin polypeptide that
XX is more active (i.e. in solution has a greater proportion of ligand-
XX forming polypeptides) than the wild-type form of the subunit. Variant

CC Integrin polypeptides of the invention are useful in assays for compounds
 CC that bind to a variant ligand, that interfere with or enhance the binding
 CC of an integrin ligand to integrin, and for identifying activation-
 CC specific ligands. They are also useful for generating antibodies, e.g.
 CC monoclonal antibodies, which bind to the high efficiency form of an
 CC integrin. Some such antibodies recognise an epitope that is either not
 CC present or not accessible on an integrin that is in a lower affinity
 CC conformation. The invention also provides methods of administering a
 CC variant integrin polypeptide, or an antibody that selectively binds it,
 CC to identify a ligand which binds to an active integrin. Such assays are
 CC useful for diagnosing inflammation, e.g. occult inflammation (e.g.
 CC abscess or an active arteriosclerotic lesion). Variant integrin
 CC polypeptides can also be used to affect the bioavailability of a variant
 CC integrin polypeptide ligand and to treat disorders associated with
 CC aberrant or unwanted integrin expression or activity, such as vascular
 CC injury.

CC Sequence 194 AA;

Query Match 99.8%; Score 974; DB 8; Length 194;
 Best Local Similarity 99.5%; Pred. No. 5.4e-99;
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CPQEDSDIAFLIDSGSIIIPHDFFRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTPK 60
 Db 1 CPQEDSDIAFLIDSGSIIIPHDFFRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTPK 60
 OY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120
 Db 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120
 OY 121 DPLGEDVIPLEADREGVIRVYIGVDARFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 Db 121 DPLGEDVIPLEADREGVIRVYIGVDARFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 OY 181 IQNQLREKFA 191
 Db 181 IQNQLREKIFA 191

RESULT 2

ID ADM99589 standard; protein; 1152 AA.

AC ADM99589;
 XX
 DT 17-JUN-2004 (first entry)

XX Human integrin alphaM subunit precursor protein.

XX integrin alpha subunit; beta; antiproliferic; thrombolytic; anticoagulant;
 KW osteopathic; cytosolic; immunosuppressive; antiinflammatory;
 KW neuroprotective; antisticking; immunotherapy; inflammation;
 KW autoimmune disorder; thrombosis; cancer; osteoporosis;
 KW sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
 KW alphaM.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Misc-difference 965
 FT /note="Encoded by CCC"

XX MO2004007530-A2.

XX 22-JAN-2004.

XX 17-JUL-2003; 2003WO-US022301.

XX 17-JUL-2002; 2002US-0396783P.

PR 17-JUL-2002; 2002US-0396790P.
 PR 11-SEP-2002; 2002US-0410135P.
 XX

PA (BL00-) CENT BLOOD RES INC.

XX Springer TA, Takagi J;

XX WPI; 2004-122877/12.

DR N-PSDB; ADM99588.

XX Novel modified integrin protein having extracellular domains of integrin
 PT alpha and beta subunits or integrin alphaII and beta3 subunit, useful for
 PT treating integrin mediated disorders.

XX Disclosure; SEQ ID NO 4; 232bp; English.

PS The invention relates to a novel isolated or recombinant modified
 CC integrin protein having extracellular domains of integrin alpha and beta
 CC subunits where one of the subunits has one or more mutations, an altered
 CC surface feature or an amino acid substitution or internal deletion,
 CC extracellular domains of the integrin beta subunit that comprise a
 CC mutation that alters a non-cysteine residue to cysteine or extracellular
 CC domains of integrin alpha and beta subunits. The polypeptide of the
 CC invention demonstrates antiproliferic, thrombolytic, anticoagulant,
 CC osteopathic, cytosolic, immunosuppressive, antinflammatory,
 CC neuroprotective and antisticking activities and may be useful for
 CC immunotherapy in order to prevent or treat an integrin-mediated disorder
 CC such as an inflammatory disorder, an autoimmune disorder, thrombosis,
 CC cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple
 CC sclerosis. The current sequence is that of the human integrin alphaM
 CC subunit precursor protein of the invention.

XX Sequence 1152 AA;

Query Match 99.8%; Score 974; DB 8; Length 1152;
 Best Local Similarity 99.5%; Pred. No. 6.5e-98;
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CPQEDSDIAFLIDSGSIIIPHDFFRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTPK 60
 Db 144 CPQEDSDIAFLIDSGSIIIPHDFFRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTPK 203
 OY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120
 Db 204 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 263
 OY 121 DPLGEDVIPLEADREGVIRVYIGVDARFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 Db 264 DPLGEDVIPLEADREGVIRVYIGVDARFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
 OY 181 IQNQLREKFA 191
 Db 324 IQNQLREKIFA 334

RESULT 3

ID ADP12435 standard; protein; 1152 AA.

AC ADP12435;

DT 12-AUG-2004 (first entry)

XX Protein encoded by mRNA of the invention #45.

XX transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

XX Homo sapiens.

XX MO2004042346-A2.

XX 21-MAY-2004.

XX 24-APR-2003; 2003WO-US012946.
 XX

SQ Sequence 1153 AA;
 Query Match 99.8%; Score 974; DB 2; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 6.5e-98;
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKKSKTLFSLMYSSEFRHPTFK 60
 DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKKSKTLFSLMYSSEFRHPTFK 203
 QY 61 EFQNNPNRSLVKEPTTOLLGRTHATGIRKVVRELFTNNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNRSLVKEPTTOLLGRTHATGIRKVVRELFTNNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGVEDVIPADREGVIRVYIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 264 DPLGVEDVIPADREGVIRVYIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
 QY 181 IQNQLREKXFA 191
 DB 324 IQNQLREKXFA 334

RESULT 5
 AAW65090
 ID AAW65090 standard; protein; 1153 AA.
 AC AAW65090;
 DT 28-SEP-1998 (first entry)
 DE Human Beta-integrin CD11b subunit protein.
 XX
 KW Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis;
 KW type-I diabetes; atherosclerosis; multiple sclerosis; asthma;
 KW lung inflammation; acute respiratory distress syndrome; CD11b subunit;
 KW rheumatoid arthritis.
 OS Homo sapiens.
 PN US5728533-A.
 PD 17-MAR-1998.
 PF 07-JUN-1995; 95US-00485618.
 PR 23-DEC-1993; 93US-00173497.
 PR 05-AUG-1994; 94US-00286889.
 PR 21-DEC-1994; 94US-00362652.
 PA (ICOS-) ICOS CORP.
 PI Van Der Vlieten M, Gallatin MM;
 DR WPI; 1998-206565/18.
 PT Screening assay for modulators of integrin binding - using immobilised or
 PT labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
 XX
 PS Example 5; Fig 1A-D; 106pp; English.
 CC This sequence represents a human beta-integrin CD11b subunit which is
 CC used to describe a method for identifying compounds that modulate the
 CC interaction of the beta-integrin alpha-d subunit with a binding partner
 CC of alpha-d which involves contacting an alpha-d polypeptide with an alpha
 CC -d binding partner, one of which is immobilised and the other of which is
 CC labelled, in the presence of a test compound, and determining if the
 CC compound affects binding between the alpha-d polypeptide and alpha-d
 CC binding partner, where the alpha-d polypeptide is alpha-d or its fragment
 CC comprising the cytoplasmic, transmembrane or extracellular domain of
 CC alpha-d. Compounds that modulate alpha-d binding could be used to treat
 CC diseases such as type-I diabetes, atherosclerosis, multiple sclerosis,
 CC asthma, psoriasis, lung inflammation, acute respiratory distress syndrome

CC and rheumatoid arthritis
 XX
 SQ Sequence 1153 AA;
 Query Match 99.8%; Score 974; DB 2; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 6.5e-98;
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKKSKTLFSLMYSSEFRHPTFK 60
 DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKKSKTLFSLMYSSEFRHPTFK 203
 QY 61 EFQNNPNRSLVKEPTTOLLGRTHATGIRKVVRELFTNNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNRSLVKEPTTOLLGRTHATGIRKVVRELFTNNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGVEDVIPADREGVIRVYIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 264 DPLGVEDVIPADREGVIRVYIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
 QY 181 IQNQLREKXFA 191
 DB 324 IQNQLREKXFA 334

RESULT 6
 AAB07360
 ID AAB07360 standard; protein; 1153 AA.
 AC AAB07360;
 DT 17-JAN-2001 (first entry)
 DE Human CD11b protein sequence.
 XX
 KW Human, macrophage infiltration inhibition; alpha-d integrin;
 KW leukocyte integrin; Leu-CAM; leukointegrin; immune response;
 KW inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes;
 KW atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin;
 KW lung inflammation; acute respiratory distress syndrome; Crohn's disease;
 KW rheumatoid arthritis; central nervous system injury; CD11b.
 OS Homo sapiens.
 PN WO200029446-A1.
 PD 25-MAY-2000.
 PF 16-NOV-1999; 99WO-USO27139.
 PR 16-NOV-1998; 98US-00193043.
 PR 08-JUL-1999; 99US-00350259.
 PA (ICOS-) ICOS CORP.
 PI Gallatin MM, Van Der Vlieten M;
 DR WPI; 2000-387751/33.
 PT Use of novel anti-alpha integrin d monoclonal antibodies to inhibit
 PT macrophage infiltration and reduce inflammation at central nervous system
 PT injury sites.
 XX
 PS Example 5; Fig 1; 270pp; English.
 CC Integrins are a class of membrane-associated molecules that participate
 CC in cellular adhesion. Integrins are made up of an alpha subunit and a
 CC beta subunit. One class of human integrins are restricted to expression
 CC in white blood cells and have a common beta2 subunit: the leukocyte
 CC integrins; Leu-CAMs, leukointegrins or beta2 integrins. Beta2 integrins
 CC have an important role in immune and inflammatory responses. The present
 CC protein sequence is the human integrin alpha subunit CD11b. This sequence
 CC was used in an alignment to identify a novel beta2 integrin alpha

CC subunit: alpha_d (AA60014 and AAB07359). The present sequence has
 CC approximately 60% identity to the protein sequence of alpha_d. The
 CC Alpha_d gene and protein may be useful in therapy for diseases linked to
 CC aberrant alpha_d function e.g. Type I diabetes, atherosclerosis, multiple
 CC sclerosis, asthma, psoriasis, lung inflammation, acute respiratory
 CC distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency
 CC (LAD). In addition, anti-alpha_d monoclonal antibodies may be used in the
 CC inhibition of macrophage infiltration at the site of a central nervous
 CC system injury. The monoclonal antibodies can also be used to detect and
 CC diagnose Crohn's disease

XX Sequence 1153 AA:

Query Match 99.8%; Score 974; DB 3; Length 1153;

Best Local Similarity 99.5%; Pred. No. 6.5e-98;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHPFRMKKEVSTVMEOLKSKTLFSIMQSEEFRIHPTFK 60
 DB 144 CPQEDSDIAFLIDGSGSIIPHPFRMKKEVSTVMEOLKSKTLFSIMQSEEFRIHPTFK 203
 QY 61 EFQNNPNPSLVKPIITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNPSLVKPIITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 263
 QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTASKPPRDHVFQVNNFEALKT 180
 DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTASKPPRDHVFQVNNFEALKT 323
 QY 181 IONQLREKKFA 191
 DB 324 IONQLREKKIFA 334

RESULT 7

AAU80252 ID AAU80252 standard; protein; 1153 AA.

XX AAU80252;

DT 15-JUL-2002 (first entry)

DE Human integrin I alpha-M subunit protein.

XX Integrin: antiinflammatory; immunosuppression; nephritis; dermatitis;

KW inflammatory disease; autoimmune disorder; Crohn's disease;

KW human immunodeficiency virus; HIV; myocardial infarction;

KW Sjogren's syndrome; rheumatoid arthritis.

XX Homo sapiens.

OS Key Location/Qualifiers

FT MISC-difference 499..500 /note="Encoded by GCG CAG AGC"

XX MO200218583-A2.

XX 07-MAR-2002.

XX 31-AUG-2001; 2001MO-US027227.

XX 01-SEP-2000; 2000US-0229700P.

XX (BLOO-) CENT BLOOD RES INC.

XX Springer TA, Shimoaka M, Lu C;

XX WPI; 2002-382964/41.

XX N-PSDB; ABK50046.

XX Modified integrin-I or integrin I-like domain polypeptide useful as an

PT immunogen to produce antibodies specific to polypeptide, comprises a

PT disulfide bond such that polypeptide is stabilized in a desired

PT conformation.

XX Disclosure; Page 109-112; 112pp; English.

PS This invention relates to a modified integrin-I or integrin I-like domain
 XX polypeptide comprising at least one disulfide bond so that the domain is
 CC stabilised in a desired conformation. The polypeptide of the invention
 CC may have antiinflammatory or immunosuppressive activities. The
 CC polypeptides of the invention have an open conformation and are useful as
 CC immunogens to produce antibodies that selectively bind to integrin I-
 CC domain; and for identifying a modulator of integrin activity, or of the
 CC interaction of an integrin and a cognate ligand. The polypeptide of the
 CC invention, or antibodies (preferably anti-LPA-1 antibody) is useful for
 CC treating or preventing an integrin mediated disorder which is an
 CC inflammatory or autoimmune disorder in a subject and for inhibiting the
 CC binding of an integrin to a cognate ligand such as Crohn's disease,
 CC nephritis; human immunodeficiency virus (HIV), myocardial infarction,
 CC Sjogren's syndrome, rheumatoid arthritis, dermatitis. A therapeutic
 CC composition comprising the peptide of the invention is useful for
 CC treating an integrin mediated disorder in a subject. The polypeptides
 CC and/or active or antigenic fragments are useful as reagents for diagnosis
 CC of integrin-mediated disorders. The present sequence represents the human
 CC polypeptides of the invention

XX Sequence 1153 AA:

Query Match 99.8%; Score 974; DB 5; Length 1153;

Best Local Similarity 99.5%; Pred. No. 6.5e-98;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHPFRMKKEVSTVMEOLKSKTLFSIMQSEEFRIHPTFK 60
 DB 144 CPQEDSDIAFLIDGSGSIIPHPFRMKKEVSTVMEOLKSKTLFSIMQSEEFRIHPTFK 203
 QY 61 EFQNNPNPSLVKPIITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNPSLVKPIITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 263
 QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTASKPPRDHVFQVNNFEALKT 180
 DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTASKPPRDHVFQVNNFEALKT 323
 QY 181 IONQLREKKFA 191
 DB 324 IONQLREKKIFA 334

RESULT 8

ABG61469 ID ABG61469 standard; protein; 1153 AA.

XX ABG61469;

DT 27-AUG-2002 (first entry)

DE Human Beta2 integrin alphaCD11b subunit;

XX Beta2 integrin; alphasubunit; CD11c subunit; CD11b subunit; LAD;

KW leukocyte adhesion deficiency; inflammatory response; diabetes;

KW multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective;

KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;

KW immune complex alveolitis; leukemia; ICAM-R; VCM-1; anti-inflammatory;

KW intracellular cell adhesion molecule; vascular cell adhesion molecule;

KW locomotor recovery; locomotor damage; locomotor impairment;

XX autonomic dysfunction; sensory dysfunction; spinal cord injury.

XX Homo sapiens.

XX MO200230980-A2.

XX 18-APR-2002.

PF 15-OCT-2001; 2001WO-US032059.
 XX 13-OCT-2000; 2000US-00688307.
 XX (ICOS-) ICOS CORP.
 XX (ICOS-) ICOS CORP.
 PI Gallatin WM, Van Der Vieren M;
 XX WPI; 2002-463260/49.
 DR
 XX
 PT Use of an anti-alpha-d monoclonal antibodies for promoting locomotor
 PT recovery, inhibiting locomotor damage, limiting locomotor impairment, or
 PT limiting autonomic and sensory dysfunction following spinal cord injury.
 XX
 XX
 PS Example 5; Page 191-194; 270pp; English.
 XX
 CC The invention relates to promoting locomotor recovery, inhibiting
 CC locomotor damage, limiting locomotor impairment, or limiting autonomic
 CC and sensory dysfunction following spinal cord injury by administering an
 CC anti-alpha-d (Betaz integrin alpha2 subunit) monoclonal antibody to a
 CC spinal cord injury victim. The method also involves the use of a ligand
 CC selected from ICM-R or VCM-1 (intracellular cell adhesion molecule,
 CC vascular cell adhesion molecule). The method is useful for promoting
 CC locomotor recovery, inhibiting locomotor damage, limiting locomotor
 CC impairment, or limiting autonomic and sensory dysfunction following
 CC spinal cord injury. In particular, the spinal cord injury comprises
 CC compression of the spinal cord. The antibodies are also useful for
 CC reducing inflammation at the site of a central nervous system injury. The
 CC specification also details the identification of Betaz integrin alphan
 CC cDNAs and proteins, for use in raising the antibodies. Betaz integrins
 CC are implicated in diseases such as LAD (leukocyte adhesion deficiency,
 CC inflammatory response, diabetes, multiple sclerosis, arthritis, graft
 CC atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative
 CC colitis, immune complex alveolitis and leukemia. The present sequence is
 CC a Betaz2 integrin alpha subunit sequence included for comparison with the
 CC Betaz2 integrin alphan protein sequences
 CC
 SQ Sequence 1153 AA;
 XX
 XX
 Query Match 99.8%; Score 974; DB 5; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 6.5e-98;
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 60
 DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 203
 QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKSRQELNTTASKPPRDVHFOVNNFEALKT 180
 DB 264 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKSRQELNTTASKPPRDVHFOVNNFEALKT 323
 QY 181 IQNQLREKXFA 191
 DB 324 IQNQLREKIFA 334

RESULT 9
 ID AAO14428
 AC AAO14428 standard; protein; 1153 AA.
 XX
 XX AAO14428;
 AC
 XX 03-MAY-2002 (first entry)
 DT
 XX
 DE Integrin Mac-1 alpha subunit.
 XX
 KM Mac-1; integrin alpha subunit; variant integrin inserted domain protein;
 KM open conformation; integrin related inflammatory disorder;
 KM integrin related immunological disorder; rheumatoid arthritis; ischaemia;
 XX

KM reperfusion; hypovolemic shock; infarctbn; cerebral shock;
 KM viral infection; cancer; gene therapy; vaccine;
 KM bioactive agent screening.
 XX
 XX Unidentified.
 XX
 XX WO200204521-A2.
 XX
 XX
 XX 17-JAN-2002.
 XX
 XX
 PF 09-JUL-2001; 2001WO-US021805.
 XX
 XX 07-JUL-2000; 2000US-0216600P.
 PR
 XX
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
 PA (BLOO-) CENT BLOOD RES.
 XX
 XX Springer T;
 XX
 DR WPI; 2002-146167/19.
 XX
 PT New integrin I domain protein having alteration in at least 2
 PT noncontiguous regions and exits in an open conformation, useful for
 PT treating, preventing or suppressing inflammatory or immunological
 PT disorders.
 XX
 XX Example 1; Fig 1F; 90pp; English.
 XX
 CC The invention comprises structurally biased variant integrin inserted (I)
 CC domain proteins, wherein the alterations to the protein occur in at least
 CC two noncontiguous regions. Specifically the variant integrin I domain
 CC proteins are structurally biased to exist in the open conformation,
 CC thereby altering the binding ability of the protein. The invention also
 CC comprises nucleic acids encoding the variant integrin I domain proteins.
 CC The integrin I domain proteins and nucleic acids are useful for treating,
 CC preventing or suppressing integrin related inflammatory and immunological
 CC disorders (e.g. Rheumatoid arthritis). The variant integrin I domain
 CC proteins and nucleic acids can also be used for treating: ischaemia/
 CC reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; viral
 CC infection; and cancer. The variant integrin I domain nucleic acids and
 CC proteins may be used in gene therapy, as vaccines and to screen for
 CC bioactive agents. The present amino acid sequence represents the Mac-1
 CC alpha subunit of integrin
 CC
 SQ Sequence 1153 AA;
 XX
 XX
 Query Match 99.8%; Score 974; DB 5; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 6.5e-98;
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 60
 DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 203
 QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKSRQELNTTASKPPRDVHFOVNNFEALKT 180
 DB 264 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKSRQELNTTASKPPRDVHFOVNNFEALKT 323
 QY 181 IQNQLREKXFA 191
 DB 324 IQNQLREKIFA 334

RESULT 10
 ID ADD25615
 AC ADD25615 standard; protein; 1153 AA.
 XX
 XX ADD25615;
 AC
 XX

15-JAN-2004 (first entry)
 Binding domain-immunoglobulin fusion protein-associated protein #85.
 Binding domain: immunoglobulin; fusion protein; associated; antidiabetic; antihypertensive; immunosuppressive; antidiabetic; antihypertensive; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
 Unidentified.
 US2003118592-A1.
 26-JUN-2003.
 25-JUL-2002; 2002US-00207655.
 17-JAN-2001; 2001US-0367358P.
 17-JUN-2002; 2002US-00053530.
 13-JUN-2002; 2002US-0385691P.
 (GENE-) GENE-CRAFT INC.
 Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 WPI; 2003-801317/75.
 New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
 Disclosure; SEQ ID NO 176; 157pp; English.
 The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide; derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain-immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification

and is also available in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docid=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
 Sequence 1153 AA;
 Query Match 99.8%; Score 974; DB 7; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 6,5e-98;
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTPK 60
 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTPK 203
 61 EFQNNPNPRLVLPITQLGRTHTATGIRKRVRELFINITNGARKNAFKLLVITDGEKFG 120
 204 EFQNNPNPRLVLPITQLGRTHTATGIRKRVRELFINITNGARKNAFKLLVITDGEKFG 263
 121 DPLGYEDVLPADRGVIRYVIGVDAPRSEKSRBELNTIASKPRDHYFOVNFELAKT 180
 264 DPLGYEDVLPADRGVIRYVIGVDAPRSEKSRBELNTIASKPRDHYFOVNFELAKT 323
 181 IONOLREKKFA 191
 324 IONOLREKIFA 334
 Db
 RESULT 11
 ADR23250
 ID ADR23250 standard; protein; 1153 AA.
 XX ADR23250;
 AC ADR23250;
 XX 04-NOV-2004 (first entry)
 DT Human integrin CD11b alpha subunit.
 XX Human integrin CD11b alpha subunit.
 DE Human; integrin; CD11b; inflammation; antiinflammatory; vasotropic.
 XX Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..16 /label= Signal_peptide
 FT Domain 144..334 /label = A_domain
 FT Misc-difference 332 /note= "Invariant Ile residue"
 FT Misc-difference 336 /note= "Invariant Glu residue"
 FT WO2004066914-A2.
 PN WO2004066914-A2.
 PD 12-AUG-2004.
 XX 12-MAY-2003; 2003WO-US014919.
 PF 10-MAY-2002; 2002US-00144259.
 PR 10-MAY-2002; 2002US-00144259.
 XX (GENE) GEN HOSPITAL CORP.
 PA Arnaud MA, Li R, Xiong J;
 PI WPI; 2004-593980/57.
 DR Novel variant integrin CD11b alpha subunit polypeptide, useful for
 PT determining candidate compound for binding to CD11b, and for determining
 PT compound as activation-dependent ligand.
 XX Claim 4; SEQ ID NO 30; 128pp; English.
 PS The present sequence is that of the human integrin alpha subunit CD11b.
 CC

CC This includes an invariant Ile residue at position 332 and an invariant
 CC Glu residue at position 336. The invention features variant integrin
 CC polypeptides comprising all or part of a variant integrin alpha subunit A
 CC domain and its flanking region. In solution or in membrane-associated
 CC form, the A domain polypeptides exist predominantly in a high affinity
 CC conformation. The variant integrin polypeptides have a crucial Ile or Glu
 CC residue either deleted or replaced by a different amino acid. Claimed
 CC polypeptides comprise: amino acids 144-336 of the present CD11b alpha
 CC subunit sequence in which the Glu-336 residue is replaced by Glu, Asp or
 CC Ala; amino acids 144-332 of the CD11b alpha subunit where the Ile-332
 CC residue is replaced by any other amino acid, especially Gly or Ala; and
 CC amino acids 144-331 of the CD11b alpha subunit sequence, but not amino
 CC acids 332-336 of this sequence. The variant integrin polypeptides
 CC selectively impair binding or activation-dependent ligands, but not
 CC independent ligands. They are useful in screening assays for the
 CC identification of molecules that enhances binding of variant polypeptides
 CC with impaired binding, and for distinguishing between activation-
 CC dependent and activation-independent ligands. They are also useful for
 CC generating antibodies, e.g. monoclonal antibodies, which bind to the
 CC impaired form of an integrin. Such antibodies recognise an epitope that
 CC is either not present or not accessible on an integrin that is in the
 CC high affinity conformation. The invention also provides methods of
 CC administering a variant integrin polypeptide, or an antibody that
 CC selectively binds it, to identify a ligand which binds to an active
 CC integrin. Such assays are useful for diagnosing inflammation, e.g. occult
 CC inflammation (e.g. abscess or an active arteriosclerotic lesion). Variant
 CC integrin polypeptides can also be used to affect the bioavailability of a
 CC variant integrin polypeptide ligand and to treat disorders associated
 CC with aberrant or unwanted integrin expression or activity, such as
 CC vascular injury.

CC Sequence 1153 AA:

Query Match 99.8%; Score 974; DB 8; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 6,5e-98;
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSITPHDFRMRKEFVSTVMEQLKSKTFLSMQYSEFRHFTFK 60
 DB 144 CPQEDSDIAFLIDSGSITPHDFRMRKEFVSTVMEQLKSKTFLSMQYSEFRHFTFK 203
 QY 61 EFQNNPNPRSLVKPTQLGRTHTATGIRKVRRELFNITNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNPRSLVKPTQLGRTHTATGIRKVRRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
 QY 181 IONQLREKXFA 191
 DB 324 IONQLREKIFA 334

RESULT 12

AAU76856
 ID AAU76856 standard; protein; 191 AA.

AC AAU76856;

DT 21-MAY-2002 (first entry)

DE Human integrin alpha subunit CD11b variant A domain.

XX Human, integrin alpha subunit; A domain; CD11b; integrin beta subunit;
 KM A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
 KM ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
 KM antiinflammatory; vasotropic; antiparasitic; vulnery; gene therapy;
 KM mutcin.

XX Homo sapiens.
 OS Synthetic.
 XX

FN Key Location/Qualifiers
 FT Misc-difference 189
 FT /label= Gly, Ala
 FT /note= "wild-type Ile substituted by Gly or Ala"

PN WO200209737-A1.

PD 07-FEB-2002.

PF 31-JUL-2001; 2001WO-US023957.

XX 31-JUL-2000; 2000US-0221950P.

PR 11-JAN-2001; 2001US-00758493.

PR 13-MAR-2001; 2001US-00805354.

XX (GENO) GEN HOSPITAL CORP.

PI Arnaout AM, Li R, Xiong J;

DR WPI; 2002-188687/24.

PT Novel high affinity integrin polypeptide useful for treating restenosis
 PT and parasitic diseases, comprises all or part of variant integrin alpha
 PT subunit A domain or variant integrin beta subunit A-like domain.

PS Claim 2; Page; 55pp; English.

CC The invention relates to a high affinity integrin polypeptide comprising
 CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for creating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC two-hybrid or three-hybrid assays. This sequence represents a human
 CC integrin alpha subunit CD11b variant A domain. Note: This variant
 CC sequence is not featured in the specification but has been derived from
 CC the wild-type protein shown in AAU76847

XX Sequence 191 AA:

Query Match 98.8%; Score 964; DB 5; Length 191;
 Best Local Similarity 98.4%; Pred. No. 6.8e-98;
 Matches 188; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSITPHDFRMRKEFVSTVMEQLKSKTFLSMQYSEFRHFTFK 60
 DB 1 CPQEDSDIAFLIDSGSITPHDFRMRKEFVSTVMEQLKSKTFLSMQYSEFRHFTFK 60
 QY 61 EFQNNPNPRSLVKPTQLGRTHTATGIRKVRRELFNITNGARKNAFKILVITDGEKFG 120
 DB 61 EFQNNPNPRSLVKPTQLGRTHTATGIRKVRRELFNITNGARKNAFKILVITDGEKFG 120
 QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 QY 181 IONQLREKXFA 191
 DB 181 IONQLREKXFA 191

RESULT 13

AAU76847
 ID AAU76847 standard; protein; 191 AA.

AC AAU76847;

XX 21-MAY-2002 (first entry)
 XX
 XX Human integrin alpha subunit CD11b A domain.
 DE
 XX Human, integrin alpha subunit; A domain; CD11b; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
 KW ischaemia-reperfusion injury; immune complex; parasitic disease;
 KW antinflammatory; vasotropic; antiparasitic; vulnery; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1.188
 FT Region /note="this region is specifically claimed"
 FT
 FT WO200209737-A1.
 PN
 XX 07-FEB-2002.
 PD
 XX 31-JUL-2001; 2001WO-US023957.
 PF
 XX 31-JUL-2000; 2000US-0221950P.
 PR 11-JAN-2001; 2001US-00758493.
 PR 13-MAR-2001; 2001US-00805354.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 XX
 XX Arnaud AM, Li R, Xiong J;
 PI
 XX WPI; 2002-188687/24.
 DR
 XX Novel high affinity integrin polypeptide useful for treating restenosis
 PT and parasitic disease, comprises all or part of variant integrin alpha
 PT subunit A domain or variant integrin beta subunit A-like domain.
 XX
 XX Example 2; Fig 5; 55pp; English.
 PS
 XX The invention relates to a high affinity integrin polypeptide comprising
 CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC two-hybrid or three-hybrid assays. This sequence represents the human
 CC integrin alpha subunit CD11b A domain
 CC
 XX
 SQ Sequence 191 AA:
 Query Match 98.8%; Score 964; DB 5; Length 191;
 Best Local Similarity 97.9%; Pred. No. 6.8e-98;
 Matches 187; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CPOEDSDIAFLIDSGSIIPHDPRMKFVSTWVQQLKSKTFLSLQYSEEFRIHFTFK 60
 DB 1 CPOEDSDIAFLIDSGSIIPHDPRMKFVSTWVQQLKSKTFLSLQYSEEFRIHFTFK 60
 QY 61 EFQNNPNPRLSVKPTQLGRTATGTRKRVRELFNTNARKNAKPAFLVINDGEKFG 120
 DB 61 EFQNNPNPRLSVKPTQLGRTATGTRKRVRELFNTNARKNAKPAFLVINDGEKFG 120
 QY 121 DPLGVEDVTPADDEGVIRYVIGVDAPRSEKSRQELNTIASKPPDHVPOVNNFEALKT 180
 DB 121 DPLGVEDVTPADDEGVIRYVIGVDAPRSEKSRQELNTIASKPPDHVPOVNNFEALKT 180
 QY 181 IQNQLREKXFA 191

DB 181 IQNQLREKXFA 191
 RESULT 14
 ID AAY21991 standard; protein; 187 AA.
 AC AAY21991;
 AC AAY21991;
 DE 13-SEP-1999 (first entry)
 DE Human complement factor MAC-1 vWF domain sequence.
 XX
 XX Factor B analogue; modified; complement activity; complement factor B;
 KW short consensus repeat domain; von Willebrand factor domain; human; C2;
 KW CR3; autoimmune response; tissue damage; lupus erythematosus; therapy;
 KW rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1;
 KW myocardial infarction; acute shock lung syndrome; inflammation; vWF.
 XX
 XX Homo sapiens.
 OS
 XX US928892-A.
 PN
 XX 27-JUL-1999.
 PD
 XX 26-JUL-1996; 96US-00687706.
 PF
 XX 03-JAN-1994; 94US-00177109.
 PR
 XX (UNITV) UNITV WASHINGTON.
 PA
 PI Oglesby TJ, Hourcade DE;
 PI
 XX WPI; 1999-429498/36.
 DR
 XX Nucleic acids encoding complement protein homologues useful for
 PT modulating function of the complement system in the treatment of a
 PT variety of immune and autoimmune complex mediated syndromes.
 XX
 XX Disclosure; Fig 5A-B; 53pp; English.
 PS
 XX The invention relates to a Factor B analogue that exhibits modified
 CC complement activity in vitro. The analogue is generated by substituting a
 CC short consensus repeat domain (SCR) or a von Willebrand factor domain
 CC (WVF) of human factor B with a SCR or a WVF from a second protein such as
 CC human C2 or CR3. The analogues may be used to regulate the complement
 CC system involved in immune and autoimmune responses. Complement activity
 CC can account for substantial tissue damage in a wide variety of autoimmune
 CC /immune complex mediated syndromes such as lupus erythematosus,
 CC rheumatoid arthritis, hemolytic anemia and myasthenia gravis. Inhibition
 CC of the complement system using the analogues is likely to provide a means
 CC of therapeutic intervention in these cases. Inhibition of complement may
 CC also be favorable in cases that involve tissue damage caused by vascular
 CC injury such as myocardial infarction, cerebral vascular accidents or
 CC acute shock lung syndrome. In these cases the complement system may
 CC contribute to the destruction of partially damaged tissue as in
 CC reperfusion injury. In addition, the use of complement analogues with
 CC novel target specificities could reduce the activity of tissue damaging
 CC proteins at sites of inflammation. Complement inhibition is important in
 CC the prevention of xenograft rejection (the inhibition of complement by
 CC cell-associated and soluble inhibitors is useful in protecting the
 CC transplant from damage caused by activation of endogenous complement. The
 CC present sequence represents the vWF domain of human factor MAC-1
 CC
 XX
 SQ Sequence 187 AA:
 Query Match 98.4%; Score 960; DB 2; Length 187;
 Best Local Similarity 100.0%; Pred. No. 1.8e-97;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPOEDSDIAFLIDSGSIIPHDPRMKFVSTWVQQLKSKTFLSLQYSEEFRIHFTFK 60

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Db      1 CPQEDSDIAFLIDSGSIIIPHDRRMKEFVSTVMEQIKKSKTLPSIMQYSEEPRIHFTPK 60
QY      61 EFQNNPNPSLVPIITQLGRTHTATGIRKRVRELNFINTGARKNAFKILVITTDKFKG 120
Db      61 EFQNNPNPSLVPIITQLGRTHTATGIRKRVRELNFINTGARKNAFKILVITTDKFKG 120
QY      121 DPLGYEDVIPLEADREGVIRYVIGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db      121 DPLGYEDVIPLEADREGVIRYVIGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
QY      181 IQNQLRE 187
Db      181 IQNQLRE 187

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QY      126 EDVIPLEADREGVIRYVIGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONOL 185
Db      132 EDVIPLEADREGVIRYVIGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONOL 191
QY      186 REKXFA 191
Db      192 REKIFA 197

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Search completed: November 8, 2005, 21:22:31
Job time : 168 secs

RESULT 15
AAB6766
ID AAB6766 standard; protein; 216 AA.

```

AC AAB6766;
DT 10-APR-2001 (first entry)
DE Amino acids 149-353 of human CR-3 alpha chain and His tag.
KW EST; expressed sequence tag; inclusion body; binding partner;
KW immunoglobulins.
OS Homo sapiens.
OS Synthetic.
PN WO200102588-A2.
XX 11-JAN-2001.
XX 30-JUN-2000; 2000WO-BP006137.
XX 02-JUL-1999; 99EP-00112815.
XX (MORP-) MORPHOSYS AG.
XX Friech C, Kretzschmar T, Hoess A, Von Rueden T;
XX WPI; 2001-147085/15.

```

Generating specific binding partners to (poly)peptides encoded by genomic DNA fragments, involves forming inclusion bodies by expressing the (poly)peptide as part of fusion proteins.

Disclosure; Page 18; 45pp; English.

The present invention relates to generating a specific binding partner to a peptide, encoded by a genomic DNA fragment or an expressed sequence tag (EST). A nucleic acid molecule encoding a fusion protein is expressed in a host cell to allow the formation of inclusion bodies comprising the fusion protein, the inclusion bodies are isolated and a specific binding partner is generated. The specific binding partners generated are useful for identifying and characterizing naturally occurring proteins e.g. as immunoglobulins or fragments in immunoassays

Sequence 216 AA;

Query Match 96.5%; Score 942; DB 4; Length 216;
Best Local Similarity 99.5%; Pred. No. 2.2e-95;
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      6 SDIAFLIDSGSIIIPHDRRMKEFVSTVMEQIKKSKTLPSIMQYSEEPRIHFTPKFQNN 65
Db      12 SDIAFLIDSGSIIIPHDRRMKEFVSTVMEQIKKSKTLPSIMQYSEEPRIHFTPKFQNN 71
QY      66 PNPSLVPIITQLGRTHTATGIRKRVRELNFINTGARKNAFKILVITTDKFKGDPDLY 125
Db      72 PNPSLVPIITQLGRTHTATGIRKRVRELNFINTGARKNAFKILVITTDKFKGDPDLY 131

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OM protein - protein search, using sw model

Run on: November 8, 2005, 20:42:47 ; Search time 39 Seconds
(without alignments)
471.215 Million cell updates/sec

Title: US-09-805-354-1

Perfect score: 976
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Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: pirl: *
2: pirl: *
3: pirl: *
4: pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	974	99.8	1153 1 RWHU1B	cell surface glyco
2	754	77.3	1153 2 S00551	leukocyte surface
3	548	56.1	1153 1 RWHU1C	cell surface glyco
4	328	33.6	1179 2 A53213	integrin alpha-E c
5	288.5	29.6	1170 2 S03308	cell surface glyco
6	266	27.3	1163 2 I56126	lymphocyte fuction
7	241	24.7	493 2 A33809	cartilage matrix p
8	234	24.0	500 2 S65522	cartilage matrix p
9	231	23.7	466 2 A37299	cartilage matrix p
10	215.5	22.1	1151 2 A45226	integrin alpha-1 c
11	215	22.0	3124 2 A40020	collagen alpha 1(X
12	214.5	22.0	1747 2 A45974	collagen alpha 1(X
13	214.5	22.0	1857 2 S31212	collagen alpha 1(X
14	214.5	22.0	1888 2 S78476	collagen alpha 1(X
15	206.5	21.2	3051 2 A42373	hypothetical prote
16	205.5	21.1	272 2 A55348	integrin alpha-1-
17	200.5	20.5	1180 2 A35854	integrin alpha-1 c
18	191.5	19.6	741 2 T46488	hypothetical prote
19	187	19.2	929 2 I51027	type XII collagen
20	174.5	17.9	2944 2 A54849	collagen alpha 1(V
21	163	16.7	3176 2 CGHU2A	collagen alpha 3(V
22	162	16.3	3137 2 A37797	collagen alpha 3(V
23	159	16.3	1170 2 A45914	integrin alpha 2 s
24	154	15.8	1181 2 A33998	integrin alpha-2 c
25	154	15.0	1178 2 S44142	VLA-2 protein homo
26	146	14.7	550 2 T23760	hypothetical prote
27	143	14.4	843 2 A40970	undulin 1 - human
28	140.5	14.4	371 2 S32604	collagen alpha 2(V
29	135.5	13.9	763 2 I50807	complement factor

30	134.5	13.8	712 2 A45638	immunodominant mic
31	132	13.5	2813 1 VWHU	von Willebrand fac
32	130.5	13.4	191 2 I47230	VLA-2 protein - p1
33	125.5	12.9	1029 1 S21369	collagen alpha 2(V
34	124.5	12.8	1022 2 S04111	collagen alpha 2(V
35	122.5	12.6	238 2 C35243	collagen alpha 2(V
36	122.5	12.6	917 2 S09646	collagen alpha 2(V
37	122.5	12.6	1018 1 CGHU2A	collagen alpha 2(V
38	119.5	12.2	724 2 A48569	antigen Em100 - B1
39	118.5	12.1	918 2 S23377	collagen alpha 2(V
40	117.5	12.0	1019 1 A32856	collagen alpha 1(V
41	115.5	11.8	427 2 G00039	von Willebrand fac
42	113.5	11.6	414 2 PS0323	complement factor
43	111	11.4	764 1 BRHU	hypothetical prote
44	109.5	11.2	567 2 T28797	hypothetical prote
45	109.5	11.2	13055 2 T16580	hypothetical prote

ALIGNMENTS

RESULT 1
RWHU1B
cell surface glycoprotein CD11b precursor [validated] - human
N:Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Ma
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1992 #sequence, revision 31-Dec-1992 #ext_change 09-Jul-2004
C:Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R:Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A>Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CR
B.
A:Reference number: A31108; MUID:88315033; PMID:2457584
A:Accession: A31108
A:Molecule type: mRNA
A:Residues: 1-1153 <COR>
A:Cross-references: UNIPROT:P11215; GB:J03925; NID:g18784; PIND:AAA5944.1; PID:g30714
A>Note: part of this sequence was confirmed by protein sequencing
R:Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A>Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor ;
A:Reference number: A28915; MUID:88257215; PMID:2454931
A:Accession: A28915
A:Molecule type: mRNA
A:Residues: 1-499,501-965, 'P', 967-1153 <ARN>
A:Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIND:AAA59
A>Note: the authors translated the codon TAC for residue 1129 as Thr
R:Shelley, C.S.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A>Title: The promoter of the CD11b gene directs myeloid-specific and developmentally re
A:Reference number: A41600; MUID:92073318; PMID:1683702
A:Accession: A41600
A:Molecule type: DNA
A:Residues: 1-9 <SHK>
A:Cross-references: GB:M76724; NID:g180018; PIND:AAA58410.1; PID:g553215
R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
A>Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhes
A:Reference number: A94193; MUID:88190151; PMID:2833753
A:Accession: A30892
A:Molecule type: mRNA
A:Residues: 917-1042 <AR2>
A:Cross-references: GB:M18044
R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A>Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence recepto
A:Reference number: A32218; MUID:89088931; PMID:2563162
A:Accession: A32218
A:Molecule type: mRNA
A:Residues: 9-1153 <HIC>
A:Cross-references: GB:J04145; NID:g189068; PIND:AAA59903.1; PID:g386975

A>Note: part of this sequence was confirmed by protein sequencing
R:Flaming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J.Immunol. 150, 480-490, 1993
A>Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in
n during evolution.
A:Reference number: A46526; MUID:93123748; PMID:8419480
A:Accession: A46526
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-499,501-1153 <FLB>
A:Cross-references: GB:IS52227; NID:9263047; PIDN:AA824821.1; PID:9263049
A:Note: the last three bases of intron 13, CAG, are included in some but not all mature
A:Accession: A46526
R:Pieper, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaud, M.A.
Biochim. Biophys. Acta 874, 368-371, 1986
A>Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp
A:Reference number: A90664; MUID:87076671; PMID:3539202
A:Accession: A26091
A:Molecule type: protein
A:Residues: 17-31 <PIB>
A:Experimental source: granulocytes
R:Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
A>Title: Characterization of the myeloid-specific CD11b promoter.
A:Reference number: 152567; MUID:92144986; PMID:1346576
A:Accession: 152567
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <RBS>
A:Cross-references: GB:M84477; NID:9180184; PIDN:AAA51960.1; PID:9553219
C:Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
C:Genetics:
A:Gene: GDB:ITGAM; CR3A
A:Cross-references: GDB:120599; OMIM:120980
A:Map position: 16p11.2-16p11.2
A>Note: promoter contains a GATA motif and two Sp1 consensus binding sites
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
C:Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>
F:17-1108/Domain: extracellular #status predicted <EXT>
F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F:465-473/Region: calcium/magnesium binding #status predicted
F:530-538/Region: calcium/magnesium binding #status predicted
F:539-601/Region: calcium/magnesium binding #status predicted
F:1109-1134/Domain: transmembrane #status predicted <TMW>
F:1135-1153/Domain: intracellular #status predicted <INT>
F:86,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding

Query Match 99.8%; Score 974; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 2,1e-75;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEQLKSKTLPFLMOWSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEQLKSKTLPFLMOWSEEFRIHFTFK 203
OY 61 EFQNNPNRSLVKTITQLGRTHTATGTRKVRRELFTNTGARKNAFILLVITDGEKFG 120
DB 204 EFQNNPNRSLVKTITQLGRTHTATGTRKVRRELFTNTGARKNAFILLVITDGEKFG 263
OY 121 DPLGVEDVTPADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVPVNNFEALKT 180
DB 264 DPLGVEDVTPADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVPVNNFEALKT 323
OY 181 IONQLREKXFA 191
DB 324 IONQLREKXFA 334

RESULT 2
S00551
leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse

N:Alternate names: complement-3 receptor alph chain
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S00551; 159078
R:Pyela, R.
EMBO J. 7, 1371-1378, 1988
A>Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the i
A:Reference number: S00551; MUID:88312584; PMID:3044779
A:Accession: S00551
A:Molecule type: DNA
A:Residues: 1-1153 <PYT>
A:Cross-references: UNIPROT:P05555; EMBL:X07640; NID:952982; PIDN:CAA30479.1; PID:952983
A:Note: the authors translated the codon CAC for residue 569 as Gln
R:Sastre, L.; Roman, J.M.; Teplov, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A>Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recep
A:Reference number: 159078; MUID:86287312; PMID:2942940
A:Accession: 159078
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 11-44 <RBS>
A:Cross-references: GB:M14293; NID:9198993; PIDN:AAA9484.1; PID:9554193
C:Genetics:
A:Gene: Mac-1
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
C:Keywords: cell adhesion; glycoprotein; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental
F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1106-1129/Domain: transmembrane #status predicted <TMW>

Query Match 77.3%; Score 754; DB 2; Length 1153;
Best Local Similarity 78.0%; Pred. No. 1.6e-56;
Matches 149; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

OY 1 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEQLKSKTLPFLMOWSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEQLKSKTLPFLMOWSEEFRIHFTFK 203
OY 61 EFQNNPNRSLVKTITQLGRTHTATGTRKVRRELFTNTGARKNAFILLVITDGEKFG 120
DB 204 DFKNPNRSHVSPKQNGRTKTAAGTRKVRRELFTNTGARKNAFILLVITDGEKFG 263
OY 121 DPLGVEDVTPADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVPVNNFEALKT 180
DB 264 DPLGVEDVTPADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVPVNNFEALKT 323
OY 181 IONQLREKXFA 191
DB 324 IONQLREKXFA 334

RESULT 3
RHWNUIC
cell surface glycoprotein CD11c precursor - human
N:Alternate names: leukocyte adhesion receptor p150,95 alpha chain
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A36584; A35433; S00864
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
A:Reference number: A36584
A:Contents: erratum
A:Accession: A36584
A:Molecule type: DNA
A:Residues: 1-1163 <COR>
A:Cross-references: UNIPROT:P20702
A:Note: this revision to the sequence from reference A35433 includes the carboxyl end
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A>Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.
A:Reference number: A35433; MUID:90153906; PMID:2303426
A:Accession: A35433

A:Molecule type: DNA
A:Residues: 1-834 <CO2>
A:Note: this sequence has been revised in reference A36584
R:CorDi, A.L.; Miller, L.O.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A:Title: CDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A:Reference number: S00864; MUID:8816645; PMID:3327687
A:Accession: S00864
A:Molecule type: mRNA
A:Residues: 1-755, V, 757-1163 <CO3>
A:Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AA59180.1; PID:g487830
A:Note: part of this sequence was confirmed by protein sequencing
C:Comment: A common beta chain, (CD18) forms a heterodimer with CD11b to form Mac-1 on my
C:Genetics:
A:Gene: GDB:ITGAX; CD11C
A:Cross-references: GDB:119758; OMIM:151510
A:Map position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
C:Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F:20-1107/Domain: extracellular #status predicted <EXT>
F:149-319/Domain: von Willebrand factor type A repeat homology <VWA4>
F:1108-1133/Domain: transmembrane #status predicted <TM>
F:1134-1163/Domain: intracellular #status predicted <INT>
F:61,89,392,697,735,899,933,1050/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 56.1%; Score 548; DB 1; Length 1163;
Best Local Similarity 56.0%; Pred. No. 7.56-39;
Matches 107; Conservative 34; Mismatches 50; Indels 0; Gaps 0;

QY 1 CPEQEDSDIAFLINGSGGIIHDPFRMKEFVSTVNWQLKKSKTLFSLMYSSEFRHIFPK 60
DB 145 CPQEQDIDYFLIDGSGSISRRNFTVMNFFVAALVISOFRPSTQSLPSNKFQTHFTFE 204
QY 61 EPCNNPNRPLVMPITLTLLKRTHTATGIRKVVRELFTNTNGARKAKAFILVVTDGKXG 120
DB 205 EFRRTSNPUSLALSVMHOLQGFYTTATAIQNVVHLLFHASYGARRATKILVITDGKKG 264
QY 121 DPLQEDVDVPEADREGVIRVYIGVGDAPRSEKSHQELNTIASKPRPDHFOVNNFEALKT 180
DB 265 DSLDQVDVIMPADAGIRRAIGVGLAFQNNNSWMLNDIASKPSQEHIFKVEDFDALKD 324
QY 181 IQNQLREKAKFA 191
DB 325 IQNQLKEKIFA 335

RESULT 4
A53213
Integrin alpha-E chain - human
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C:Accession: A53213
R:Shaw, S.K.; Ceppek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.
J. Biol. Chem. 269, 6016-6025, 1994
A:Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit. U
A:Reference number: A53213; MUID:94164962; PMID:8119947
A:Accession: A53213
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1179 <SHA>
A:Cross-references: UNIPROT:P38570; GB:I25851; NID:g457244; PID:g457245
C:Genetics:
A:Gene: GDB:ITGAE
A:Cross-references: GDB:330801
A:Map position: 17p13
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
F:199-371/Domain: von Willebrand factor type A repeat homology <VWA3>

Query Match 33.6%; Score 328; DB 2; Length 1179;
Best Local Similarity 38.8%; Pred. No. 5.76-20;
Matches 71; Conservative 42; Mismatches 68; Indels 2; Gaps 1;

QY 6 SDIAFLIDSGSIIIPHDFRMKEFVSTVMEQL--KSKTLFSLMOYSEEFRIHFTKEPQ 63

Db 201 TEIAIILIDGSGSIDPPDFQAKXDFISNMKNFYEKCECNFALVQGVQVITQTEFDLDSQ 260

QY 64 NNPNPSLIVNPITQOLGRHTATGIRKVVRELFINITNGARKNAFKILVITIDSEKFGDPL 123

Db 261 DNASLARVONITQVGSVITKTAAMQVHLDISITSSHGSRKRSKVMVVLTDGIGFEDPL 320

QY 124 GYEDVPEADREAGIRGVICDAFRSEKSRQEIINTIASRPPDHVQVNNFEALKTION 183

Db 321 NLTIVNSPKQGVVERAIGVGEEFMSARIRARELNIIASDPDETHAFKVTNNYALDGLLS 380

QY 184 QLR 186

Db 381 KLR 383

RESULT 5

S03308

cell surface glycoprotein CD11a precursor - human

N.Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function

C.Species: Homo sapiens (man)

C.Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004

C.Accession: S03308; A47458; A48759; S36044

R.Iarson, R.S.; Corbi, A.L.; Berman, L.; Springer, T.

J. Cell Biol. 108, 703-712, 1989

A.Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit

A.Reference number: S03308; MUID:89139587; PMID:2557322

A.Accession: S03308

A.Molecule type: mRNA

A.Residues: 1-1170 <L>R>

A.Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:g31421; PIDN:CAA68

A.Note: part of this sequence was confirmed by protein sequencing

R.Cornwell, R.D.; Gollahan, K.A.; Hirstein, D.D

Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993

A>Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) pr

A.Reference number: A47458; MUID:93248261; PMID:8097887

A.Molecule type: DNA

A.Residues: 1-20 <COR>

A.Note: sequence extracted from NCBI backbone (NCBIN:130862, NCBI:P:130863)

R.Shelley, C.S.; Farokhzad, O.C.; Arnaout, M.A.

Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993

A>Title: Identification of cell-specific and developmentally regulated nuclear factors

A.Reference number: A47565; MUID:93281759; PMID:8099450

A.Accession: A47565

A.Molecule type: DNA

A.Residues: 1-20 <SH>

A.Cross-references: GB:M95609

R.Nueda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.

J. Biol. Chem. 268, 19305-19311, 1993

A>Title: Characterization of the CD11a (alphaL, LFA-1alpha) integrin gene promoter.

A.Reference number: A48759; MUID:93374910; PMID:8103515

A.Molecule type: DNA

A.Residues: 1-20 <NU>

A.Cross-references: EMBL:Z22804; NID:g311405; PIDN:CAA80461.1; PID:g311406

C.Genetics:

A.Gene: GDB:ITGAL; CD11A

A.Cross-references: GDB:119757; OMIM:153370

A.Map position: 16p11.2-16p11.2

C.Superfamily: cell surface glycoprotein CD11b, von Willebrand factor type A repeat hom

C.Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; tr

F.1-25/Domains: signal sequence #status predicted <SIG>

F.26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted

F.154-311/Domains: von Willebrand factor type A repeat homology <VWA>

Query Match 29.6%; Score 288.5; DB 2; Length 1170;

Best Local Similarity 32.6%; Pred. No. 1,4e-16;

Matches 62; Conservative 50; Mismatches 71; Indels 7; Gaps 2;

1 CQEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTPFK 60

```
Db      150 CTKGVADVLFVFDGSMISLPDEFQKILDFMKQVMKLTNTSYQFAAVQFSTSYKTEPDFS 209
Qy      61 EFQNNPNRSLVLPKPTQLGRTHTATGIRKVRRELFNTNGARKNAFKILVITDGEKFG 120
Db      210 DYVKKKDDPDLKHKHMLLNTLNGALNYVATEFRRELGRPRPATVLLITDGE--A 267
Qy      121 DPLGVEDVTPADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db      268 TDSGNIDAKD-----IIRYIIIGIKHPTQKESQGLTKHKFASKPASEFVKILDTETKXD 322
Qy      181 IQNQLREKCF 190
Db      323 LFTLELQKKIY 332
```

```
RESULT 6
156126
Lymphocyte function-associated molecule-1-alpha - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 156126
R/Kaufmann, Y.; Teeng, E.; Springer, T.A.
J. Immunol. 147, 369-374, 1991
A/Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit a
A/Reference number: 156126; MUID:91268576; PMID:2051027
A/Accession: 156126
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1163 <RES>
A/Cross-references: UNIPROT:P24063; GB:M60778; NID:G198785; PIDN:AAA39426.1; PID:G198786
C/Genetics:
A/Gene: LFA-1
C/Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homology
P:151-315/Domain: von Willebrand factor type A repeat homology <VWA1>
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```
Query Match      27.3%; Score 266; DB 2; Length 1163;
Best Local Similarity 32.2%; Pred. No. 1.2e-14;
Matches 64; Conservative 40; Mismatches 73; Indels 22; Gaps 3;

Qy      1 CPQESDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTLPSLMQYSEEFRIHFTPEK 60
Db      147 CMKGKVDLVFLFDGSLDRKDFEKILFEMDVMKLSNTSYQFAAVQFSTDCRTEPFL 206
Qy      61 EF-QNNPNRSLVLPKPTQLGRTHTATGIRKVRRELFNTNGARKNAFKILVITDGEK 119
Db      207 DYVKKKDDPDLKHKHMLLNTLNGALNYVATEFRRELGRPRPATVLLITDGE-- 263
Qy      120 GDPLEGVEDVTPADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQV 172
Db      264 -----EASDKGNISAAHDITRYIIIGIKHPTQKESQGLTKHKFASKPASEFVKIL 312
Qy      173 NNFEALKTIQNQLREKCA 191
Db      313 DTETKXDLPDLKHKHMLLNTLNGALNYVATEFRRELGRPRPATVLLITDGE-- 331
```

```
RESULT 7
A33809
Cartilage matrix protein precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C/Accession: A33809; A26364
R/Klas, I.; Deak, F.; Hollway Jr., R.G.; Delius, H.; Meubst, K.A.; Frimberger, E.; Argz
J. Biol. Chem. 264, 8126-8134, 1989
A/Title: Structure of the gene for cartilage matrix protein, a modular protein of the ex
grins, von Willebrand factor, complement factors B and C2, and epidermal growth factor.
A/Reference number: A33809; MUID:89255246; PMID:2542265
A/Accession: A33809
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-493 <KIS>
A/Cross-references: UNIPROT:P05099; GB:X12346; GB:X12347; GB:X12348; GB:X12349; GB:X1235
```

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R/Argaves, W.S.; Deak, F.; Sparkes, K.J.; Kiehl, I.; Goettinck, P.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A/Title: Structural features of cartilage matrix protein deduced from cDNA.
A/Reference number: A26364; MUID:87092429; PMID:3025875
A/Accession: A26364
A/Molecule type: mRNA
A/Residues: 78-493 <ARG>
A/Cross-references: GB:M4792; NID:G211545; PIDN:AAA48695.1; PID:G211546
C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
F:337-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F:225-260/Domain: EGF homology <EGF>
F:270-434/Domain: von Willebrand factor type A repeat homology <VWA2>
```

```
Query Match      24.7%; Score 241; DB 2; Length 493;
Best Local Similarity 31.4%; Pred. No. 5.6e-13;
Matches 59; Conservative 38; Mismatches 73; Indels 18; Gaps 4;

Qy      7 DIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTLPSLMQYSEEFRIHFTPEK 64
Db      272 DLVFLIDSGSKVRDENFELVKFINGIVESLESEKQAVGLVQSSVRQEPFLGQPKN 331
Qy      65 NNPNRSLVLPKPTQLGRTHTATGIRKVRRELFNTNGARKNAFKILVITDGEKFGDPLG 124
Db      332 KKDIAKAVKXKMAVMEKGMTGQALKYVDSFSIANGARPGVPVGIPTDGRS----- 385
Qy      125 YEDVTPADRE---GVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db      386 -QDYITDAKAKAKDLGFRMPAVGVGNV-----EDLEIREIASEVVAEHVFTADPRTISN 439
Qy      181 IQNQLREK 188
Db      440 IGRKLQMK 447
```

```
RESULT 8
566522
Cartilage matrix protein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: 566522
R/Abzodi, A.; Hauser, N.; Studer, D.; Paulsach, M.; Hirtl, L.; Bosse, Z.
Eur. J. Biochem. 236, 970-977, 1996
A/Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein c
A/Reference number: 566522; MUID:96270751; PMID:8665920
A/Accession: 566522
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-500 <AS2>
A/Cross-references: UNIPROT:P51942; EMBL:U35035; NID:G1163178; PIDN:AA06521.1; PID:G116
C/Genetics:
A/Gene: CMP
C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-500/Product: cartilage matrix protein #status predicted <MAT>
F:43-210/Domain: von Willebrand factor type A repeat homology <VWA1>
F:231-266/Domain: EGF homology <EGF>
F:277-441/Domain: von Willebrand factor type A repeat homology <VWA2>
```

```
Query Match      24.0%; Score 234; DB 2; Length 500;
Best Local Similarity 29.6%; Pred. No. 2.3e-12;
Matches 56; Conservative 44; Mismatches 71; Indels 18; Gaps 4;

Qy      6 SDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTLPSLMQYSEEFRIHFTPEK 63
Db      278 TDVFLIDSGSKVRDENFELVKFINGIVESLESEKQAVGLVQSSVRQEPFLGQPKN 337
Qy      64 NNPNRSLVLPKPTQLGRTHTATGIRKVRRELFNTNGARKNAFKILVITDGEKFGDPL 123
Db      338 SKDIDKARVNMMSWMEGTMGALKYLINSFVSSGARPGAKVGIVFTDGRS----- 392
Qy      124 GYEDVTPADRE---GVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALK 179
Db      393 -QDYINDAKAKAKDLGFRMPAVGVGNV-----EEDLEIREIASEVVAHDHYFTADPFTIN 445
```

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OY      180 TIONOLREK 188
      446 QIGKTLQKK 454
Db

RESULT 9
cartilage matrix protein precursor - human
A:Species: Homo sapiens (man)
C:Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004
C:Accession: A37979; B37979
R:Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh
J. Biol. Chem. 265, 19624-19631, 1990
A:Title: Structure and chromosomal location of the human gene encoding cartilage matrix
A:Reference number: A37979; MUID:91060568; PMID:2246248
A:Accession: A37979
A:Molecule type: DNA
A:Residues: 1-496 <JEN>
A:Cross-references: UNIPROT:P31941; GB:J05667
A:Accession: B37979
A:Molecule type: mRNA
A:Residues: 137-290, 'L', 292-496 <JEN>
A:Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PID:G
A:Gene: GDB:CRIM
A:Cross-references: GDB:127280; OMIM:115437
A:Map position: 1p35-1p35
A:Intron: 33/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C:Complex: homotrimer
C:Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-96/Product: cartilage matrix protein #status predicted <MAT>
F:227-262/Domain: von Willebrand factor type A repeat homology <VWA1>
F:273-437/Domain: EGF homology <EGF>
F:273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F:176-344/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:221-236,234-247,249-262/Distal/Disulfide bonds: #status predicted

Query Match      23.7%; Score 231; DB 2; Length 496;
Best Local Similarity 29.6%; Pred. No. 4, 1e-12;
Matches 56; Conservative 42; Mismatches 73; Indels 18; Gaps 4;

OY      6 SDIAFLIDSGSIIPDPRMKEFSTVMEOLKSKTL--FSIMQYSEEFRIHFTKEPQ 63
      274 TDVFLIDSGSKSRPEFELVKFISQIDYTLVSDKLAQVGLVQISSVROEFPFGRH 333
Db
OY      64 NNENPSRLVKPIITQLGRTHTATGIRKRVNELFNITNGARKNAFKILVITDGEKFGDPL 123
      334 TKKDIAAARVMNMYMEGTMGTGAALKYLIDNSFTVSSGAPGAQKGVITDGRS----- 388
Db
OY      124 GVEDVTPPEADRE---GVIRIVYGVGDPAFSEKSRQELNTIAKPRPDHVFQVNNFEAL 179
      389 --ODYINDAKKAKDLGFKMFAVGAVNAV-----EDELREIASEPVAEHFYADPKTIN 441
Db
OY      180 TIONOLREK 188
      442 QIGKTLQKK 450
Db

RESULT 10
A45226
Integrin alpha-1 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45226
R:Bliesewitz, R.; Epstein, M.R.; Marcantonio, E.E.
J. Biol. Chem. 268, 2989-2996, 1993
A:Title: Expression of native and truncated forms of the human integrin alpha 1 subunit.
A:Reference number: A45226; MUID:9315124; PMID:8428973
A:Accession: A45226
A:Status: preliminary; not compared with conceptual translation

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A:Molecule type: mRNA
A:Residues: 1-1151 <BRI>
A:Cross-references: UNIPROT:P56199
A:Experimental source: hepatoblastoma cell line HepG2
A>Note: sequence extracted from NCBI backbone (NCBI:124326)
F:142-317/Domain: von Willebrand factor type A repeat homology <VWA1>

Query Match      22.1%; Score 215.5; DB 2; Length 1151;
Best Local Similarity 30.6%; Pred. No. 2, 5e-10;
Matches 59; Conservative 38; Mismatches 85; Indels 11; Gaps 5;

OY      7 DIAFLIDSGSIIPDPRMKEFSTVMEOLK--KSKTLFSIMQYSEEFRIHFTKEPQ 64
      144 DIVYLDSSNSITPMD--SVTRFLNDLKRMDIGKQOVGVQYGVNTHFNLKXSS 201
Db
OY      65 NNENPSRLVKPIITQLGR--THATGIRKRVNELFNITNGARKNAFKILVITDGEKFGDPL 123
      202 TEEVVAAKKIIVQRGGRQMTALGTDARKEAFTRAGARGVKVMYIVTDGESH--DNH 260
Db
OY      124 GVEDVTPPEADREGVIRIVYGVGDAR-----SEKSRQELNTIAKPRPDHVFQVNNFEAL 178
      261 RLKRVIOCEEDENIQRFSAIAGSYNRGNTLSTEKVEEIKSLASEPTEKHFVNSDELAL 320
Db
OY      179 KTIQNLREKXPA 191
      321 VTIKTLGERIPA 333
Db

RESULT 11
A40020
collagen alpha 1(XII) chain precursor - chicken
N:Alternate names: fibrochimerin
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
R:Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Oba
U. Cell Biol. 115, 209-221, 1991
A:Title: The complete primary structure of type XII collagen shows a chimeric molecule
A:Reference number: A40020; MUID:92011862; PMID:1918137
A:Accession: A40020
A:Molecule type: mRNA
A:Residues: 1-3124 <YAM>
A:Cross-references: UNIPROT:P31944; GB:D00824; NID:g222810; PIDN:BA00701.1; PID:g22281;
A>Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and
R:Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A:Title: Type XII collagen: A large multidomain molecule with partial homology to type
A:Reference number: A34485; MUID:90062079; PMID:2584192
A:Accession: A34485
A:Molecule type: mRNA
A:Residues: 2456-2758, 'A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>
A:Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A:Accession: B34485
A:Molecule type: protein
A:Residues: 2772-2792; 2846-2873 <GOR2>
A:Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A:Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA
A:Reference number: A28037; MUID:87317590; PMID:3476925
A:Accession: A28037
A:Molecule type: mRNA
A:Residues: 2960-2976, 'F', 2978-3074, 'AG', <GOR3>
A:Cross-references: EMBL:M7375; NID:g211649; PIDN:AAA48718.1; PID:g211650
R:Koch, M.; Bernasconi, C.; Chiquet, M.
Eur. J. Biochem. 207, 847-856, 1992
A:Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of
A:Reference number: S23814; MUID:92362621; PMID:1323460
A:Accession: S23814
A:Molecule type: protein
A:Residues: 'X', 1333, 'O', 1335-1347; 1914-1928; 2504, 'X', 2506, 'X', 2508-2511, 'X', 2513-2517
R:Dublet, B.; van der Rest, M.

```


QY	DB	Query Match	Best Local Similarity	22.0%	Score 215	DB 2	Length 3124
QY	Db	6 SDIAFLIDGSGSIIIPHDRFMKEFVSTWME--QLKSKTFLSLNQYSEEFPIHFTPEFQ 63	30.6%	Pred. No. 9.6e-10			
QY	Db	138 TDVFLVNDGSSVGNANRRYILDFVNLVLSAFDGEETRKGVOYSSDPTTEENLNQYF 197	37	Mismatches 74	Indels 18	Gaps 4	
QY	Db	64 NNPNRSLVKPDTQLGLTHTATGIRKVRLEFNITNGARRNAFKLIVITDGKFGDPL 123					
QY	Db	198 RRSLLDAIKRIPIYKGGTMTGEALDYLVKMTFTESAGARQPKVAIVITDGKA----- 252					
QY	Db	124 GYEVNIPADE----GYIRVIVIGGDAFREKSKROELNTIASRPRPHVQUNNEALK 179					
QY	Db	253 --QBEVLPAAELRNIGVEVSLGIKAA----DAKEIKLLIASPSLKHVNVNVAWFGVIT 305					

QY 180 TIONQL 185
Db 306 DIQNEI 311

RESULT 12
A45974
collagen alpha 1(XIV) chain precursor, short form 2 - chicken

N/Alternate names: undulin
C/Species: Gallus gallus (chicken)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A45974 #sequence: 522916; S17035; S20833
R/Gene: R. R.; Foley, J. W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin
J. Biol. Chem. 268, 12177-12184, 1993
A/Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region
na.
A/Reference number: A45974; MUID:93280195; PMID:8505337
A/Accession: A45974

A/Status: preliminary
A/Molecule type: mRNA, protein
A/Residues: 1-1747 <GER>
A/Cross-references: UNIPROT:P32018
A/Experimental source: embryo skin
A/Note: sequence inconsistent with the nucleotide translation
A/Note: sequence extracted from NCBI backbone (NCBI:133364, NCBI:133365)
R/Apte, S.S.
submitted to the EMBL Data Library, March 1992
A/Reference number: S30085
A/Accession: S30085
A/Molecule type: mRNA
A/Residues: 1472-1660 <APT>
A/Cross-references: EMBL:X65122; NID:G62871; PIDN:CAA46238.1; PID:G938175
R/Trueb, U.; Trueb, B.
Eur. J. Biochem. 207, 549-557, 1992
A/Title: Type XIV collagen is a variant of undulin.
A/Reference number: S22916; MUID:92339443; PMID:1339349
A/Accession: S22916

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 286-494, 'Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 <TRU>
R/Gordon, M. K.; Castagnola, P.; Dublet, B.; Linsmeayer, T. F.; van der Rest, M.; Mayne,
Eur. J. Biochem. 201, 333-338, 1991
A/Title: Cloning of a cDNA for a new member of the class of fibrin-associated collagens
A/Reference number: S17035; MUID:92037585; PMID:1935930
A/Accession: S17035
A/Molecule type: mRNA
A/Residues: 1472-1659 <GOR1>
A/Accession: S20833

A/Molecule type: protein
A/Residues: 1551-1570, 1593-1599, 1639-1667 <GOR2>
C/Keywords: alternative splicing; coll; extracellular matrix; glycoprotein; trimer
F/40-204/Domain: von Willebrand factor type A repeat homology <VMA1>
F/236-317/Domain: fibronectin type III repeat homology <FMA3>
F/326-409/Domain: fibronectin type III repeat homology <FMA3>
F/418-498/Domain: fibronectin type III repeat homology <FMA3>
F/507-591/Domain: fibronectin type III repeat homology <FMA3>
F/625-707/Domain: fibronectin type III repeat homology <FMA3>
F/716-798/Domain: fibronectin type III repeat homology <FMA3>
F/806-893/Domain: fibronectin type III repeat homology <FMA3>
F/924-1089/Domain: von Willebrand factor type A repeat homology <VMA2>
F/1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>
F/1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F/1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>

Query Match 22.0%; Score 214.5; DB 2; Length 1747;
Best Local Similarity 32.4%; Pred. No. 5.1e-10;
Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;

QY 1 CPOESDIAFLIDSGSIIIPHDFRMKEFY-STV--MEQKKSKTLFSLIMQYSEEFRIHF 57
Db 920 CCAAKADLVFLVDGSHSGIDGNPNKIIISFLYSTVGALDKIGPDGTQVAIIIGFSDDPRIEF 979

58 TPKERQNNENPRLSVLPITQLGRTHTATGIRKVRLEFNITNGARKNAFKILLVITDGE 117

Db 980 KLNAYKTELTLEAIOQLAYKGNKTKKAIKHAREVFTGBAGRKGIIPKVLVITDGR 1039
Qy 118 KFGDPLGVEDVYPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVOVNNEA 177
Db 1040 SODD---VNKYSREMQLDGFSFPAIGVADADYS-----ELVNIGSKPSERHVFVDDIDA 1091
Qy 178 LKTIONQL 185
Db 1092 FTKIEDEL 1099

RESULT 13

S31212
C:Species: Gallus gallus (chicken)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
C:Accession: S31212
R:Mauchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A:Title: Complete primary structure of chicken collagen XIV.
A:Reference number: S31211; MUID:93185668; PMID:844186
A:Accession: S31212
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-1857 <MAE>
A:Cross-references: EMBL:X70792; NID:9288874; PINN:CA50063.1; PID:9288875
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C:Genetics:
A:Gene: COL14A1
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>
F:29-110/Domain: fibronectin type III repeat homology <FN3A>
F:156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
F:352-433/Domain: fibronectin type III repeat homology <FN3B>
F:442-525/Domain: fibronectin type III repeat homology <FN3C>
F:534-614/Domain: fibronectin type III repeat homology <FN3D>
F:623-707/Domain: fibronectin type III repeat homology <FN3E>
F:741-823/Domain: fibronectin type III repeat homology <FN3F>
F:832-914/Domain: fibronectin type III repeat homology <FN3G>
F:922-1009/Domain: fibronectin type III repeat homology <FN3H>
F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 22.0%; Score 214.5; DB 2; Length 1857;
Best Local Similarity 32.4%; Pred. No. 5.5e-10;
Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;
Db 1036 CAAAKADLVFLVDGWSIGDDNFNKIISFLYSTVGLDKIGPDGVOVALIQSDDPRTTF 1095
Qy 58 TPKFQNNPNPSLVKPIITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGE 117
Db 1096 KLNAYKTELTLEAIOQLAYKGNKTKKAIKHAREVFTGBAGRKGIIPKVLVITDGR 1155
Qy 118 KFGDPLGVEDVYPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVOVNNEA 177
Db 1156 SODD---VNKYSREMQLDGFSFPAIGVADADYS-----ELVNIGSKPSERHVFVDDIDA 1207

Qy 178 LKTIONQL 185
Db 1208 FTKIEDEL 1215

RESULT 14
S78476
C:Species: Gallus gallus (chicken)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S78476; S31211
R:Trueb, B.
submitted to the EMBL Data Library, January 1993

A:Reference number: S78476
A:Accession: S78476
A:Molecule type: mRNA
A:Residues: 1-1888 <TRU>
A:Cross-references: UNIPROT:P32018; EMBL:X70793; NID:9288872; PINN:CA50064.1; PID:92888
R:Mauchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A:Title: Complete primary structure of chicken collagen XIV.
A:Reference number: S31211; MUID:93185668; PMID:844186
A:Accession: S31211
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1416;1460-1811, 1843-1888 <MAE>
A:Cross-references: EMBL:X70793
C:Genetics:
A:Gene: COL14A1
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F:29-110/Domain: fibronectin type III repeat homology <FN3A>
F:156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
F:352-433/Domain: fibronectin type III repeat homology <FN3B>
F:442-525/Domain: fibronectin type III repeat homology <FN3C>
F:534-614/Domain: fibronectin type III repeat homology <FN3D>
F:623-707/Domain: fibronectin type III repeat homology <FN3E>
F:741-823/Domain: fibronectin type III repeat homology <FN3F>
F:832-914/Domain: fibronectin type III repeat homology <FN3G>
F:922-1009/Domain: fibronectin type III repeat homology <FN3H>
F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 22.0%; Score 214.5; DB 2; Length 1888;
Best Local Similarity 32.4%; Pred. No. 5.6e-10;
Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;
Db 1036 CAAAKADLVFLVDGWSIGDDNFNKIISFLYSTVGLDKIGPDGVOVALIQSDDPRTTF 1095
Qy 58 TPKFQNNPNPSLVKPIITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGE 117
Db 1096 KLNAYKTELTLEAIOQLAYKGNKTKKAIKHAREVFTGBAGRKGIIPKVLVITDGR 1155
Qy 118 KFGDPLGVEDVYPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVOVNNEA 177
Db 1156 SODD---VNKYSREMQLDGFSFPAIGVADADYS-----ELVNIGSKPSERHVFVDDIDA 1207

Qy 178 LKTIONQL 185
Db 1208 FTKIEDEL 1215

RESULT 15
S42373
C:Species: Caenorhabditis elegans
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004
C:Accession: S42373
R:Smith, A.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42368
A:Accession: S42373
A:Molecule type: DNA
A:Residues: 1-3051 <SMI>
A:Cross-references: EMBL:Z30423; NID:9458479; PID:9458485
C:Genetics:
A:Intron: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;
F:512-679/Domain: von Willebrand factor type A repeat homology <VWA1>
F:754-793/Domain: fibronectin type II repeat homology <2F1>
F:1201-1244/Domain: EGF homology <EGF>

Query Match 21.2%; Score 206.5; DB 2; Length 3051;
Best Local Similarity 31.7%; Pred. No. 5e-09;
Matches 63; Conservative 40; Mismatches 71; Indels 25; Gaps 8;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 8, 2005, 20:47:13 ; Search time 177 Seconds
(without alignments)
552.583 Million cell updates/sec

Title: US-09-805-354-1
Perfect score: 976
Sequence: 1 CPQEDSDIAFLIDSGSIIP.....VNFEALKTIONQREKKFA 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97.4	99.8	1152	1 ITAM_HUMAN	P11215 homo sapien
2	78.7	80.6	920	2 Q28984	Q28984 sus scrofa
3	75.4	77.3	1153	1 ITAM_MOUSE	P05555 mus musculu
4	72.7	74.5	1151	2 Q6J130	Q91310 rattus norv
5	60.9	62.4	205	2 Q63001	Q63001 rattus norv
6	60.3	61.8	1161	1 ITAD_RAT	Q9qye7 rattus norv
7	59.1	60.6	1162	1 ITAD_HUMAN	Q13349 homo sapien
8	54.8	56.1	1163	1 ITAX_HUMAN	P20702 homo sapien
9	54.2	55.5	1188	2 Q6KAS4	Q6ka44 mus musculu
10	54.1	55.4	1169	1 ITAX_MOUSE	Q9qxr4 mus musculu
11	40.8	41.8	304	2 Q6PG66	Q6pg66 mus musculu
12	34.3	35.1	895	2 Q9WUF8	Q9wuf8 mus sp. Itg
13	34.3	35.1	1167	2 Q88340	Q88340 rattus norv
14	34.1	34.9	1038	2 Q8BS01	Q8bs01 mus musculu
15	33.7	34.5	1167	1 ITAE_MOUSE	Q60677 mus musculu
16	32.8	33.6	1179	1 ITAE_HUMAN	P38570 homo sapien
17	32.6	33.0	1160	2 Q8MKF4	Q8mkf4 felis silve
18	32.5	33.0	1167	2 Q88341	Q88341 rattus norv
19	31.9	32.7	231	2 Q8N882	Q8n882 homo sapien
20	30.2	30.9	79	2 Q8HY27	Q8hy27 ovis aries
21	30.2	30.9	79	2 Q8HY41	Q8hy41 bos taurus
22	292.5	30.0	1170	1 ITAL_HUMAN	P20701 homo sapien
23	285.5	29.3	1165	1 ITAL_BOVIN	P61625 bos taurus
24	280	28.7	269	2 Q8WES9	Q8wes9 rattus norv
25	266	27.3	1160	2 Q9R200	Q9r200 mus musculu
26	266	27.3	1161	2 Q9WTV4	Q9wtv4 mus musculu
27	265.5	27.2	1163	1 ITAL_MOUSE	P24063 mus musculu
28	261.5	26.8	1166	2 Q6TYB8	Q6tyb8 bos taurus
29	251.5	25.8	1187	2 Q98TF0	Q98tf0 cyprinus ca
31	24.7	25.3	257	2 Q8C270	Q8c270 mus musculu

32	241	24.7	493	1	CAMA_CHICK	P05099 gallus gall
33	237	24.3	652	2	Q9SLT2	Q9slt2 bos taurus
34	234	24.0	500	1	CAMA_MOUSE	P51942 mus musculu
35	234	24.0	500	2	Q8OVN5	Q8ovn5 mus musculu
36	231	23.7	496	1	CAMA_HUMAN	P21941 homo sapien
37	231	23.7	656	2	Q96DT1	Q96dt1 homo sapien
38	231	23.7	678	2	Q9UDN0	Q9udn0 homo sapien
39	231	23.7	693	2	Q96DM8	Q96dm8 homo sapien
40	226.5	23.2	1086	2	Q96HB1	Q96hb1 homo sapien
41	222.5	22.8	589	2	Q7ZX63	Q7zx63 xenopus lae
42	222.5	22.8	755	2	Q00261	Q00261 homo sapien
43	222.5	22.8	956	2	Q99K64	Q99k64 mus musculu
44	221	22.6	650	2	Q8VH15	Q8vh15 mus musculu
45	220.5	22.6	915	2	Q6UWAS	Q6uwas homo sapien

ALIGNMENTS

RESULT 1
ITAM_HUMAN
ID ITAM_HUMAN STANDARD; PRT; 1152 AA.
AC P11215;
DT 01-JUN-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (leukocyte adhesion receptor) (Neutrophil adherence receptor).
DE Name=ITGAM; Synonyms=CD11B, CR3A;
OS Homo sapiens (Human)
OC Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88315033; PubMed=2457584;
RA Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
RT "The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B.";
RT J. Biol. Chem. 263:12403-12411(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=883190151; PubMed=2833753;
RA Arnaout M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.;
RT "Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mo1: chromosomal localization and homology to the alpha subunits of integrins";
RT Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88257215; PubMed=2454931; DOI=10.1083/jcb.106.6.2153;
RA Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
RT "Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mo1 (complement receptor type 3).";
RT J. Cell Biol. 106:2153-2158(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=9313748; PubMed=8419480;
RA Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
RT "Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during evolution.";
RT J. Immunol. 150:480-490(1993).
RN [5]
RP SEQUENCE OF 9-1153 FROM N.A.
RX MEDLINE=89098893; PubMed=2563162;
RA Hickey D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L., Roth G.J.;
RT "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
RN [6]
RN SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=92073318; PubMed=1683702;
RA Shelley C.S., Arnaut M.A.,
RT "The promoter of the CD11b gene directs myeloid-specific and
RT developmentally regulated expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
RN [7]
RN SEQUENCE OF 1-9 FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=92144986; PubMed=1346576;
RA Pahl H.L., Rosemarin A.G., Tenen D.G.,
RT "Characterization of the myeloid-specific CD11b promoter.";
RL Blood 79:865-870(1992).
RN [8]
RN SEQUENCE OF 17-31.
RX MEDLINE=87076671; PubMed=3539202; DOI=10.1016/0167-4838(86)90037-3;
RA Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaut M.A.,
RT "N-terminal sequence of human leukocyte glycoprotein Mol: conservation
RT across species and homology to platelet Iib/Iiia.";
RL Biochim. Biophys. Acta 874:368-371(1986).
RN [9]
RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
RX MEDLINE=95171458; PubMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
RA Lee J.O., Rieu P., Arnaut M.A., Liddington R.,
RT "Crystal structure of the A domain from the alpha subunit of integrin
RT CR3 (CD11b/CD18)." ;
RL Cell 80:631-638(1995).
RN [10]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
RX MEDLINE=96363671; PubMed=8747460; DOI=10.1016/S0969-2126(01)00271-4;
RA Lee J.O., Bankston L.A., Arnaut M.A., Liddington R.C.,
RT "Two conformations of the integrin A-domain (I-domain): a pathway for
RT activation?";
RL Structure 3:1333-1340(1995).
RN [11]
RN X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
RX MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;
RA Baldwin E.T., Saver R.W., Bryant G.L. Jr., Curry K.A.,
RA Faltbanks M.B., Finzel B.C., Garlick R.L., Heinrichson R.L.,
RA Horton N.C., Kelley L.L., Milder A.M., Moon U.B., Mott J.E.,
RA Mutchler V.T., Tomich C.S., Matempaugh K.D., Wiley V.H.,
RT "Calcium binding to the integrin CD11b I domain and activation model
RT assessment." ;
RL Structure 6:923-935(1998).
RN [12]
RN 3D-STRUCTURE MODELING OF 17-616.
RX MEDLINE=98226734; PubMed=9560195; DOI=10.1073/pnas.95.9.4870;
RA Oxyvig C., Springer T.A.,
RT "Experimental support for a beta-propeller domain in integrin alpha-
RT subunits and a calcium binding site on its lower surface." ;
RL Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).
RN [1]
RN FUNCTION: Integrin alpha-M/beta-2 is implicated in various
RN adhesive interactions of monocytes, macrophages and granulocytes
RN as well as in mediating the uptake of complement-coated particles.
RN It is identical with CR-3, the receptor for the ICB fragment of
RN the third complement component. It probably recognizes the R-G-D
RN peptide in Cb β . Integrin alpha-M/beta-2 is also a receptor for
RN fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
RN of fibrinogen gamma chain.
RN [2]
RN SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
RN associates with beta-2.
RN [3]
RN SUBCELLULAR LOCATION: Type I membrane protein.
RN [4]
RN TISSUE SPECIFICITY: Predominantly expressed in monocytes and
RN granulocytes.
RN [5]
RN DOMAIN: The integrin I-domain (inset) is a VMPA domain. Integrins
RN with I-domains do not undergo protease cleavage.
RN [6]
RN SIMILARITY: Belongs to the integrin alpha chain family.
RN [7]
RN SIMILARITY: Contains 7 FG-GAP repeats.
RN [8]
RN SIMILARITY: Contains 1 VMPA domain.
RN [9]
RN DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
RN WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".

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CC -----
DR EMBL; J03925; AAA59544.1; -;
DR EMBL; M18044; AAA59491.1; -;
DR EMBL; U04145; AAA59903.1; -;
DR EMBL; S52227; AAB24821.1; -;
DR EMBL; S52152; AAB24821.1; JOINED
DR EMBL; S52153; AAB24821.1; JOINED
DR EMBL; S52154; AAB24821.1; JOINED
DR EMBL; S52155; AAB24821.1; JOINED
DR EMBL; S52157; AAB24821.1; JOINED
DR EMBL; S52159; AAB24821.1; JOINED
DR EMBL; S52161; AAB24821.1; JOINED
DR EMBL; S52164; AAB24821.1; JOINED
DR EMBL; S52165; AAB24821.1; JOINED
DR EMBL; S52167; AAB24821.1; JOINED
DR EMBL; S52169; AAB24821.1; JOINED
DR EMBL; S52170; AAB24821.1; JOINED
DR EMBL; S52173; AAB24821.1; JOINED
DR EMBL; S52174; AAB24821.1; JOINED
DR EMBL; S52180; AAB24821.1; JOINED
DR EMBL; S52181; AAB24821.1; JOINED
DR EMBL; S52184; AAB24821.1; JOINED
DR EMBL; S52189; AAB24821.1; JOINED
DR EMBL; S52191; AAB24821.1; JOINED
DR EMBL; S52192; AAB24821.1; JOINED
DR EMBL; S52203; AAB24821.1; JOINED
DR EMBL; S52212; AAB24821.1; JOINED
DR EMBL; S52213; AAB24821.1; JOINED
DR EMBL; S52216; AAB24821.1; JOINED
DR EMBL; S52219; AAB24821.1; JOINED
DR EMBL; S52220; AAB24821.1; JOINED
DR EMBL; S52221; AAB24821.1; JOINED
DR EMBL; S52222; AAB24821.1; JOINED
DR EMBL; S52226; AAB24821.1; JOINED
DR EMBL; M76724; AAA58410.1; -;
DR EMBL; M84477; AAA51960.1; -;
DR PIR; A31108; RMH11B.
DR PDB; 1A8X; Model; @=17-1152.
DR PDB; 1BHO; X-ray; 1/2=-;
DR PDB; 1BHQ; X-ray; 1/2=-;
DR PDB; 1IDQ; X-ray; 1/2=-;
DR PDB; 1IDQ; X-ray; @=140-331.
DR PDB; 1JDM; X-ray; @=143-334.
DR PDB; 1JMU; X-ray; A=137-331.
DR PDB; 1MF7; X-ray; A=144-337.
DR PDB; 1N92; X-ray; A=140-335.
DR PDB; 1NA5; X-ray; A=144-345.
DR Genew; HGNC:6149; ITGAM.
DR MIM; 120980; -;
DR GO; GO:0008305; C:integrin complex; TAS.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR InterPro; IPR000413; Integrin_alpha.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VMA; 1.
DR PRINTS; PRO1185; INTEGRIN.
DR PRINTS; PRO0453; WFPADOMAIN.
DR SMART; SMO0191; Int_alpha; 5.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VMPA; 1.
DR 3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
KW Transmembrane.

FT	SIGNAL	1	16	Integrin alpha-M.
FT	CHAIN	17	1152	
Query Match			99.8%;	Score 974; DB 1; Length 1152;
Best Local Similarity			99.5%;	Pred. No. 1,1e-70;
Matches 190;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	1	CPQEDSDIAFLIDSGSIIIPHDPRFMKEFVSTWNEQLKSKTILFSLMOYSEEPRIHFTFK	60	
DB	144	CPQEDSDIAFLIDSGSIIIPHDPRFMKEFVSTWNEQLKSKTILFSLMOYSEEPRIHFTFK	203	
QY	61	EFQNNPNRSLVKPITOLLGRTHRTATGRKRVYRELFTTNGARKNAFKILVITDGEKFG	120	
DB	204	EFQNNPNRSLVKPITOLLGRTHRTATGRKRVYRELFTTNGARKNAFKILVITDGEKFG	263	
QY	121	DPLGEDVTPPADRGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVQVNNFEALKT	180	
DB	264	DPLGEDVTPPADRGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVQVNNFEALKT	323	
QY	181	IONOLREKCKFA 191		
DB	324	IONOLREKIFFA 334		
RESULT 2				
Q28984				
ID	Q28984	PRELIMINARY;	PRT;	920 AA.
AC	Q28984;			
DT	01-NOV-1996	(TREMBLrel. 01. Created)		
DT	01-FEB-1997	(TREMBLrel. 02. Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24. Last annotation update)		
DE	CD11b (Fragment)			
GN	Name=CD11b;			
OS	Sus scrofa (Pig)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxId=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RV	Lee J.-K., Schook L.B., Rutherford M.S.;			
RL	Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).			
CC	-1- SIMILARITY: Belongs to the Integrin alpha chain family.			
DR	EMBL; U40072; AAB16869.1; -			
DR	HSSP; P11215; INAS.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0008305; C:protein complex; IEA.			
DR	GO; GO:0005515; F:protein binding; IEA.			
DR	GO; GO:0007160; P:cell-matrix adhesion; IEA.			
DR	GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.			
DR	InterPro: IPR000413; Integrin_alpha.			
DR	InterPro: IPR002035; VWF_A.			
DR	Pfam: PF00092; VWA; 1.			
DR	PRINTS; PRO185; INTEGRINA.			
DR	PRINTS; PRO0453; VWFADOMAIN.			
DR	SMART; SM00191; Int_alpha; 4.			
DR	SMART; SM00327; VWA; 1.			
DR	PROSITE; PSS0234; VWF_A; 1.			
KW	Cell adhesion; Integrin; Transmembrane.			
FT	NON_TER	1		
FT	NON_TER	920		
SO	SEQUENCE	920 AA;	102440 MW;	E96CC51E350DD5AC CRC64;
Query Match		80.6%;	Score 787;	DB 2; Length 920;
Best Local Similarity		80.6%;	Pred. No. 1,5e-55;	
Matches 154;	Conservative	18;	Mismatches 19;	Indels 0; Gaps 0
QY	1	CFQEDSDIAFLIDSGSIIIPHDPRFMKEFVSTWNEQLKSKTILFSLMOYSEEPRIHFTFK	60	
DB	11	CFQEDSDIAFLIDSGSIIIPHDPRFMKEFVSTWNEQLKSKTILFSLMOYSEEPRIHFTFK	70	
QY	61	EFQNNPNRSLVKPITOLLGRTHRTATGRKRVYRELFTTNGARKNAFKILVITDGEKFG	120	

Db 71 DFKRNPSPKLVLRPIRQLGRRHTATGIRKRVRELPHSGSARENALKILVITDGEKEG 130

Qy 121 DPLGVEDVTPPADREGVIRYVIGVGDAFSSSEKSRQELNTITASKPPDDHYPQVNNFEALKT 180

Db 131 DPLGVEDVTPPADRGKGVIRYVIGVGDAFNSWKSREBLNTITASKPCGDHVPQNNFEAVKT 190

Qy 181 IONOLRECKFA 191

Db 191 IONOLQEKTFP 201

RESULT 3

ITAM_MOUSE

ID ITAM_MOUSE STANDARD; PRT; 1153 AA.

AC P05555; Q8CA73;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (leukocyte adhesion receptor MO1).

GN Name:Itgam;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=88312584; PubMed=3044779;

RA Pyela R.;

RT "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor.";

RL EMBO J. 7:1371-1378 (1988).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC STRAIN=C57BL/6J; TISSUE=Spinal cord;

RX MEDLINE=22354663; PubMed=12466851; DOI=i0.1038/nature01266;

RA Okazaki I., Futuno M., Kasukawa T., Adachi U., Bono H., Kondo S., Nikaado I., Osebo N., Saito R., Suzuki H., Yamana H., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojopori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schirml L.M., Kampin A., Matsuda H., Batalov S., Beisels K.W., Blake J.A., Bradt D., Brusic V., Chothia G., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrester A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Guethlin S., Hirokawa N., Jackson J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., Lyons P.A., Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Ling B.L., Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pearce G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravalet T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sanderlin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Tóssdale R.D., Tomita M., Verardo R., Wagner L., Welterstedt C., Wang Y., Wetlande Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yamagata M., Yang I., Yang L., Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirocane-Kishikawa T., Kono H., Nakamura M., Sakezune N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda K., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kigawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino Y., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;

RT "Analysis of the mouse Transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).

RN [3]

RP SEQUENCE OF 11-45 FROM N.A.

RX STRAIN=BALB/c; TISSUE=Spleen;

RC MEDLINE=66287312; PubMed=2942940;

RA Sætre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E., Larson R.S., Roberts T.M., Springer T.A.;

RT "A partial genomic DNA clone for the alpha subunit of the mouse

RT complement receptor type 3 and cellular adhesion molecule Mac-1.",
RT Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
RN [4]
RP SEQUENCE OF 17-28.
RA MEDLINE=85188276; PubMed=3887182;
RX Springer T.A., Teplow D.B., Dreyer W.J.;
RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
RT glycoproteins and unexpected relation to leukocyte interferon.";
RL Nature 314:540-542(1985).
CC -1- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
CC adhesive interactions of monocytes, macrophages and granulocytes
CC as well as in mediating the uptake of complement-coated particles.
CC It is identical with CR-3, the receptor for the iC3b fragment of
CC the third complement component. It probably recognizes the R-G-D
CC peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
CC fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
CC of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in
CC glomerulonephritis. Mice expressing a null mutation of the alpha-M
CC subunit gene demonstrate increase in neutrophil accumulation, in
CC response to a impaired degranulation and phagocytosis, events that
CC apparently accelerate apoptosis in neutrophils. These mice develop
CC obesity.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
CC associates with beta-2.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing, Named isoforms=2;
CC Name=1;
CC IsoId=P05555-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P05555-2; Sequence=VSP_010473;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
CC granulocytes.
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.
CC -1- SIMILARITY: Contains 1 VWFA domain.
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CC -----
DR EMBL; X07640; CAA30479.1; -;
DR EMBL; AK039444; BAC30350.1; -;
DR EMBL; M14293; AAA39484.1; -;
DR F1R; S00551; S00551.
DR HSP; P11215; 1BHQ.
DR MGD; G619607; Itgam.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0007155; P:cell adhesion; IMP.
DR GO; GO:0045123; P:cellular extravasation; IMP.
DR GO; GO:0030593; P:neutrophil chemotaxis; IMP.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP_3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA_1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; WFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS00234; VWFA; 1.
KW Alternative splicing; Calcium; Cell adhesion;
KW Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
KW Signal; Transmembrane.

FT	SIGNAL	1	16
FT	CHAIN	17	1153
FT	DOMAIN	1106	1129
FT	TRANSMEM	1106	1129
FT	DOMAIN	1130	1153
FT	REPEAT	31	84
FT	REPEAT	85	163
FT	DOMAIN	154	350
FT	REPEAT	337	400
FT	REPEAT	401	452
FT	REPEAT	454	515
FT	REPEAT	517	575
FT	REPEAT	580	632
FT	CA_BIND	465	473
FT	CA_BIND	529	537
FT	CA_BIND	592	600
FT	SITE	1132	1136
FT	DISULFID	66	73
FT	DISULFID	105	123
FT	DISULFID	654	711
FT	DISULFID	770	776
FT	DISULFID	999	1023
FT	DISULFID	1028	1033
FT	CARBOHYD	58	58
FT	CARBOHYD	86	86
FT	CARBOHYD	391	391
FT	CARBOHYD	696	696
FT	CARBOHYD	724	724
FT	CARBOHYD	772	772
FT	CARBOHYD	801	801
FT	CARBOHYD	881	881
FT	CARBOHYD	907	907
FT	CARBOHYD	941	941
FT	CARBOHYD	980	980
FT	CARBOHYD	994	994
FT	CARBOHYD	1022	1022
FT	CARBOHYD	1045	1045
FT	CARBOHYD	1051	1051
FT	CARBOHYD	1076	1076
FT	VARSPLIC	453	569
FT	CONFLICT	37	37
FT	CONFLICT	683	683
FT	SEQUENCE	1153 AA; 127480 MW; 178DB98BAECB0343 CRC64;	
SO	SEQUENCE		
Query Match			
Best Local Similarity 77.3%; Score 754; DB 1; Length 1153;			
Matches 149; Conservative 19; Mismatches 23; Indels 0; Gaps 0;			
QY	1	CPQESDIAFLIDSGSITPHDFRMKKEFVSIVMEQLKSKSTLFSIMQYSEFRIFHTFK	60
DB	144	CPQESDIAFLIDSGSININIDFQMKKEFVSIVMEQFKSKSTLFSIMQYSEFRIFHTFN	203
QY	61	EFQNNPSPSLVYPITQILGRTHYATGIRKVVRELFTNTGARKAKFKLLVITDGEKRG	120
DB	204	DFKRNPSPRSHVSPITQILNGRTKTAGIRKVVRELFTHTKNGARENKAKLLVITDGEKRG	263
QY	121	DLGLGVEDVPEADREGVIRYVGVGDAFSEKSRQRLNTTAKPPPDHYFOVNNFEALKT	180
DB	264	DPLDVKDVIPEADRGVIRYVGVGDAFSEKSRRELDTTASPAGEHVFQVDFEALNT	323
QY	181	IONOLREKKFA 191	
DB	324	IONOLREKKFA 334	
RESULT 4			
ID	09J130	PRELIMINARY;	PRT; 1151 AA.
AC	09J130;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		

```

DE Integrin beta 2 alpha subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Fathallah D.M. Sr., Zeria K. Jr.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I/membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AF268593; AAF81280.1; -.
DR HSSP; P1215; 1BHQ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR000413; Intergrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PRO1185; INTEGRINA.
DR PRINTS; PRO0453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS00334; VWF_A; 1.
DR Cell adhesion; Integrin; Transmembrane.
SQ SEQUENCE 1151 AA; 126943 MW; 8F785695D4074C45 CRC64;

Query Match 74.5%; Score 727; DB 2; Length 1151;
Best local Similarity 74.3%; Pred. No. 1.5e-50;
Matches 142; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

OY 1 CPQEDSDIAFLIDSGSIIPHDFRRMKEFVSTWEQLKKSKTLFSLWYSEFRIHPTFK 60
DB 144 CPQGSNIAFLIDSGSINTIDFQMKKEFVSTWMDQFOKSKTLFSLWYSEDFRTHFTFN 203
OY 61 EFQNNPNRSLVKEPTTOLLGRHTHTATGRKVVRELFNTNCRKAKFAKILVITIDGKEG 120
DB 204 DFKRNPDPKSHVRPIROLNGRTKTSAGIRKVVRELFQKINGARDAAKILVITIDGKEG 263
OY 121 DPLGVEDIPEADREGVIRYVGVGDAPFSEKSRQELNTISKSPRPDHVQVNNFEALKT 180
DB 264 DPLNYEDIPEAEKGITRIYVIGVNAFHKPSQRRELDITISKSPAGDHVQVNDFEALNT 323
OY 181 IQNQLREKXFA 191
DB 324 IRNQLQEKIFA 334

RESULT 5
O63001 PRELIMINARY; PRT; 205 AA.
AC O63001
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Integrin alpha-M (Fragment).
GN Name=Itgam;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Nabika T., Ito T., Kitada H., Serikawa T., Mahino T., Soudrier F.,
RA Jullier C., Maeda J., Yamori Y., Nara Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL; U59801; AAB03226.1; -.
DR HSSP; P1215; 1BHO.

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DR GO; GO:0007229; P: Integrin-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF000092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
DR Integrin.
KW NON_TER
FT NON_TER
SQ SEQUENCE 205 AA; 22922 MW; C6C2D9395008DA36 CRC64;

Query Match 62.4%; Score 609; DB 2; Length 205;
Best Local Similarity 74.7%; Pred. No. 9e-42;
Matches 121; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

OY 30 VSTMEDQKSKTLFSIMQYSEERFHFPEKFNQNNPNPSLVKPTTOLLGRTATGIR 89
DB 1 VSTMEDQKSKTLFSIMQYSEERFHFPEKFNQNNPNPSLVKPTTOLLGRTATGIR 60
OY 90 KVARELFNITNGARKNAFKLLVITDQEKFGDPLGYEDVPEADREGVIRYVIGVDAR 149
DB 61 KVARELFQKINGARDNAKLLVITDQEKFGDPLVEDVPEAREAGIIRYVIGVANA 120
OY 150 SEKSROELNTASKRPDHYFQNNFPAKLTIONOLREKFA 191
DB 121 KQSRRELDITASKPDGHDVQVDNFALNTINNOLEKIFA 162

RESULT 6
ITAD_RAT ID ITAD_RAT STANDARD; PRT; 1161 AA.
AC O9Q0Y7;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor.
Name=Itgad;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
(1)
SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley;
RA O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietech G.,
Gallatin W.M.;
RL "Cloning of rat alpha D, a novel beta 2 integrin.";
Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
VCAM1. May play a role in the atherosclerotic process such as
clearing lipoproteins from plaques and in phagocytosis of blood-
borne pathogens, particulate matter, and senescent erythrocytes
from the blood (By similarity).
CC -I- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
associates with beta-2 (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -I- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
with I-domains do not undergo protease cleavage.
CC -I- SIMILARITY: Belongs to the integrin alpha chain family.
CC -I- SIMILARITY: Contains 7 FG-GAP repeats.
CC -I- SIMILARITY: Contains 1 VWFA domain.
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the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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DR EMBL; AF021334; AAF21241.1; -.
DR HSSP; P11215; IIRHO.
DR InterPro; IPR000413; Integrin_alpha.

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DR InterPro: IPR002035; VWF_A.
DR Pfam: PRO0357; EG-GAP; 3.
DR Pfam: PRO0357; Integrin_alpha; 1.
DR Pfam: PRO0092; VWA; 1.
DR PRINTS: PRO1185; INTEGRINA.
DR SMART: SM00191; VWFDOMAIN.
DR SMART: SM00327; VWA; 5.
DR PROSITE: PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE: PS0234; VWF; 1.
DR PROSITE: PS0234; Integrin; Integrin; Magnesium; Receptor;
KW Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1161 Integrin alpha-D.
FT DOMAIN 20 1100 Extracellular (Potential).
FT TRANSMEM 1101 1121 Potential.
FT DOMAIN 1122 1161 Cytoplasmic (Potential).
FT REPEAT 34 87 FG-GAP 1.
FT REPEAT 88 7 FG-GAP 2.
FT REPEAT 152 334 VWF.
FT DOMAIN 152 402 FG-GAP 3.
FT REPEAT 403 454 FG-GAP 4.
FT REPEAT 456 517 FG-GAP 5.
FT REPEAT 519 577 FG-GAP 6.
FT REPEAT 582 634 FG-GAP 7.
FT CA_BIND 467 475 Potential.
FT CA_BIND 531 539 Potential.
FT CA_BIND 594 602 Potential.
FT SITE 1126 1130 GEFGR motif.
FT DISULFID 69 76 By similarity.
FT DISULFID 108 126 By similarity.
FT DISULFID 656 711 By similarity.
FT DISULFID 769 775 By similarity.
FT DISULFID 845 860 By similarity.
FT DISULFID 993 1017 By similarity.
FT DISULFID 1022 1027 By similarity.
FT CARBOHYD 61 61 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 696 696 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 784 784 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 907 907 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 936 936 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1045 1045 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1161 AA; 126600 MW; 2258491A984A705B CRC64;

Query Match 61.8%; Score 603; DB 1; Length 1161;
Best Local Similarity 61.3%; Pred. No. 2e-40;
Matches 117; Conservative 30; Mismatches 44; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHPRNKEFVSTVMEOLKSKTLPFSLMOYSEEFRIHPTK 60
DB 146 CPQEDMDIFLIDGSGSINORDPAQKMDPKALMGSEFASTSTLFSIMQYSNLIKTHFTPT 205
QY 61 EFQNNNPASIVKPIQQLGRTHTATGIRKRVRELNINNGARKNAFKLIIVITDSEKRG 120
DB 206 EFNINIDPQSLVDPIVQLGSLTTATGIRKRWELPHSKNGSKSKKILLVITDQOKR 265
QY 121 DPLGVEDVTPADRECVIRYVIGVGDAFSEKSRQELNTASKPPRDHYFOVNNFEALKT 180
DB 266 DPLEVSDVTPADKAGITIRYALIGVDAFDEPTAKLKLNTIGASPPQDHYFKVGNFALNS 325
QY 181 IONQREKKFA 191
DB 326 IOROLOEKIFA 336

RESULT 7
ITAD_HUMAN STANDARD; PRT; 1162 AA.
AC Q13349; Q15575; Q15576;

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DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor (Leukointegrin alpha D) (CD11d) (ADB2).
OS Homo sapiens (Human).
GN Name=ITGAD;
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE= spleen;
RX MEDLINE=96111956; PubMed=8777714; DOI=10.1016/1074-7613(95)90058-6;
RA Van der Vlieten M., Le Trong H., Wood C.L., Moore P.F., St John T.,
RT Staunton D.E., Gallatin W.M.;
RT "A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-3."
RT Immunity 3:683-690(1995).
RN [2]
RP SEQUENCE OF 1-235 FROM N.A.
RX MEDLINE=20187620; PubMed=10722744; DOI=10.1074/jbc.275.12.8959;
RA Noti J.D., Johnson A.K., Dillon J.D.;
RT "Structural and functional characterization of the leukocyte integrin gene CD11d. Essential role of Sp1 and Sp3."
RL J. Biol. Chem. 275:8959-8969(2000).
RN [3]
RP SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A.
RX MEDLINE=9657236; PubMed=8666289; DOI=10.1016/0378-1119(95)00869-1;
RA Wong D.A., Davis E.M., Lebeau M., Springer T.A.;
RT "Cloning and chromosomal localization of a novel gene-encoding a human beta 2-integrin alpha subunit."
RL Gene 171:291-294(1996).
RN [4]
RP INTERACTION WITH VCAM1.
RX MEDLINE=99059842; PubMed=9841932;
RA Grayson M.H., Van der Vlieten M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Staunton D.E., Bochner B.S.;
RT "alpha-defensin 2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-1)."
RL J. Exp. Med. 188:2187-2191(1998).
RN [5]
RP INTERACTION WITH VCAM1.
RX MEDLINE=99370002; PubMed=10438935;
RA Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
RT "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a binding interface between I domain and VCAM-1."
RL J. Immunol. 163:1984-1990(1999).
CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of blood-borne pathogens, particulate matter, and senescent erythrocytes from the blood.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell lines and subsets of peripheral blood leukocytes and strongly on tissue-specialized cells, including macrophages foam cells within atherosclerotic plaques, and on splenic red pulp macrophages.
CC -!- DOMAIN: The integrin I-domain (inset) is a VWF domain. Integrins with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWF domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/

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FT CA_BIND 467 475 Potential.
 RT CA_BIND 531 539 Potential.
 FT CA_BIND 594 602 Potential.
 FT SITE 1140 1144 GPRK motif.
 FT DISULFID 69 76 By similarity.
 FT DISULFID 108 126 By similarity.
 FT DISULFID 656 711 By similarity.
 FT DISULFID 770 776 By similarity.
 FT DISULFID 858 873 By similarity.
 FT DISULFID 1007 1031 By similarity.
 FT DISULFID 1036 1041 By similarity.
 FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 267 267 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 949 949 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1059 1059 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1084 1084 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 1169 AA; 129150 MW; C616412033C219A6 CRC64;

Query Match 55.4%; Score 541; DB 15; Length 1169;
 Best Local Similarity 55.0%; Pred. No. 2.3e-35;
 Matches 105; Conservative 32; Mismatches 54; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTLPFSIMQSEEFRIHFTFK 60
 DB 146 CPQODDIYFLIDSGSISSTDFEKMDFVKAMVSQLQRPSTRFSLMPSDYFRVHFTFN 205
 QY 61 EQNNPNPRLSVKPTIQLGRTHTATGIRKVRBELNITNGARKNAFKLIVITTDSEKRG 120
 DB 206 NFISTSSPLSLGVSQRLGRTYTAIAKRVITELFTTOSGARQDXTKVLIVITTDGRKOG 265
 QY 121 DPLGYEDVPEADREGVIRYVIGVGDAPFSEKSRQELNTIASKPRPDHYFOVNNFEALTK 180
 DB 266 DNLSTDSVTPMAEASIIIRYALGVGKAFVNEHSEKQELKALIASPSHEHYVFSVENFDALDO 325
 QY 181 IONQLREKXFA 191
 DB 326 IENQLKEKIFA 336

RESULT 11
 Q6PG66 PRELIMINARY; PRT; 304 AA.
 AC 06PG66;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Integrin alpha X.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBITaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Smetten C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,
 RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Sherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RA Straubeberg R.;
 RL Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL, BC057200; AAH57200.1; -
 DR GO, GO:0007229; P: Integrin-mediated signaling pathway; IEA.
 DR InterPro, IPR02035; VWF_A.
 DR Pfam, PF00092; VWF_1.
 DR PRINTS, PR00453; VWFADOMAIN.
 DR SMART, SM00327; VWA; 1.
 DR PROSITE, PS50234; VWF_A; 1.
 KW Integrin.
 SQ SEQUENCE 304 AA; 33404 MW; EC52F3EAA48FA068D CRC64;

Query Match 41.8%; Score 408; DB 2; Length 304;
 Best Local Similarity 53.3%; Pred. No. 3.5e-25;
 Matches 80; Conservative 25; Mismatches 43; Indels 2; Gaps 1;

QY 1 CPQEDSDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTLPFSIMQSEEFRIHFTFK 60
 DB 146 CPQODDIYFLIDSGSISSTDFEKMDFVKAMVSQLQRPSTRFSLMPSDYFRVHFTFN 205
 QY 61 EQNNPNPRLSVKPTIQLGRTHTATGIRKVRBELNITNGARKNAFKLIVITTDSEKRG 120
 DB 206 NFISTSSPLSLGVSQRLGRTYTAIAKRVITELFTTOSGARQDXTKVLIVITTDGRKOG 265
 QY 121 DPLGYEDVPEADREGVIRYVIGVGDAPFSEKSRQELNTIASKPRPDHYFOVNNFEALTK 180
 DB 266 DNLSTDSVTPMAEASIIIRYALGVGKAFVNEHSEKQELKALIASPSHEHYVFSVENFDALDO 325

RESULT 12
 Q9WUP8 PRELIMINARY; PRT; 895 AA.
 AC 09WUP8;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Itgae protein (Fragment).
 GN Name=Itgae;
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBITaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schoen M.P., Arya A., Murphy E.A., Adams C.M., Strach U.G.,
 RA Agace W.W., Marzel J., Donohue J.P., Her H., Beier D.R., Olson S.,
 RA LeFrancis L., Brenner M.B., Grusby M.J., Parker C.M.;
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
 DR EMBL, AF133085; AAD30063.1; -
 DR EMBL, AF133070; AAD30063.1; JOINED.
 DR EMBL, AF133071; AAD30063.1; JOINED.
 DR EMBL, AF133072; AAD30063.1; JOINED.
 DR EMBL, AF133073; AAD30063.1; JOINED.
 DR EMBL, AF133074; AAD30063.1; JOINED.
 DR EMBL, AF133075; AAD30063.1; JOINED.
 DR EMBL, AF133076; AAD30063.1; JOINED.
 DR EMBL, AF133077; AAD30063.1; JOINED.
 DR EMBL, AF133078; AAD30063.1; JOINED.
 DR EMBL, AF133079; AAD30063.1; JOINED.
 DR EMBL, AF133080; AAD30063.1; JOINED.
 DR EMBL, AF133081; AAD30063.1; JOINED.
 DR EMBL, AF133082; AAD30063.1; JOINED.
 DR EMBL, AF133083; AAD30063.1; JOINED.
 DR EMBL, AF133084; AAD30063.1; JOINED.


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RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RT Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20530913; PubMed=1076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagata T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Iehi Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL: AC040983; BAC30769.1; -.
DR HSSP: P11215; 1BHQ.
DR MGD: MGI:1298377; Itgae.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0016021; C:integral to membrane; TAS.
DR InterPro: IPR000413; C:integral to membrane; TAS.
DR InterPro: IPR002035; VWF A.
DR Pfam: PF00092; VWA; 1.
DR PRINTS: PR01185; INTEGRINA.
DR PRINTS: PR00453; VWFADOMAIN.
DR SMART: SM00191; Int alpha; 4.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS50234; VWFA; 1.
DR Cell adhesion; Integrin; Transmembrane.
DR SEQUENCE 1038 AA; 114722 MW; 2B1BE7660795587 CRC64;
SQ

```

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ID ITAE MOUSE STANDARD; PRT; 1167 AA.
AC 060677;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-E precursor (Integrin alpha M290).
GN Name=Itgae;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MKR;
RX MEDLINE=95187992; PubMed=7882170; DOI=10.1016/1074-7613(94)90070-1;
RA Smith T.J., Ducharme L.A., Shaw S.K., Parker C.M., Brenner M.B.,
RA Kilshaw P.J., Wells J.H.;
RT "Murine M290 integrin expression modulated by mast cell activation.";
RT Immunity 1:393-403(1994).
CC -1- FUNCTION: Integrin alpha-E/beta-7 is a receptor for E-cadherin. It
CC mediates adhesion of intra-epithelial T-lymphocytes to epithelial
CC cell monolayers. Mice expressing a null mutation of the alpha-E
CC subunit gene exhibit a marked reduction in the numbers of
CC intraepithelial lymphocytes in the gut and in the development of
CC gut-associated lymphoid aggregates, supporting a specific role for
CC this integrin in mediating retention of lymphocytes in the
CC intestinal wall.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. The alpha
CC subunit is composed of an heavy and a light chains linked by a
CC disulfide bond. Alpha-E associates with beta-7.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
CC -1- SIMILARITY: Contains 5 FG-GAP repeats.
CC -1- SIMILARITY: Contains 1 VWFA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U12236; AAC52142.1; -.
DR HSSP: P11215; 1BHQ.
DR MGD: MGI:1298377; Itgae.
DR InterPro: IPR000413; Integrin_alpha.
DR InterPro: IPR002035; VWF A.
DR Pfam: PF01839; FG-GAP; 3.
DR Pfam: PF00357; Integrin_alpha; 1.
DR Pfam: PF00092; VWA; 1.
DR PRINTS: PR01185; INTEGRINA.
DR PRINTS: PR00453; VWFADOMAIN.
DR SMART: SM00191; Int alpha; 4.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS50242; INTEGRIN_ALPHA; 1.
DR PROSITE: PS50234; VWFA; 1.
DR Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 19
FT CHAIN 20 1167 By similarity.
FT CHAIN 20 181 Integrin alpha-E, light chain.
FT CHAIN 183 1167 Integrin alpha-E heavy chain.
FT DOMAIN 20 1114 Extracellular (Potential).
FT TRANSMEM 1115 1137 Potential.
FT DOMAIN 1138 1167 Cytoplasmic (Potential).
FT DOMAIN 149 192 X-domain (extra domain).
FT DOMAIN 193 384 VWFA.
FT REPEAT 394 448 FG-GAP 1.
FT REPEAT 449 501 FG-GAP 2.
FT REPEAT 503 564 FG-GAP 3.

```

RESULT 15
ITAE_MOUSE

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FT REPEAT 566 631 FG-GAP 4.
FT REPEAT 634 686 FG-GAP 5.
FT CA_BIND 514 522 Potential.
FT CA_BIND 578 586 Potential.
FT CA_BIND 646 654 Potential.
FT DOMAIN 185 191 Glu-rich (acidic).
FT SITE 1140 1144 GFPK motif.
FT DISULFID 72 83 By similarity.
FT DISULFID 130 164 By similarity.
FT DISULFID 698 754 By similarity.
FT DISULFID 814 820 By similarity.
FT DISULFID 884 898 By similarity.
FT DISULFID 998 1023 By similarity.
FT DISULFID 1031 1047 By similarity.
FT CARBOHYD 51 51 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 314 314 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 341 341 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 364 364 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 418 418 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 437 437 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 718 718 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 773 773 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 829 829 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 846 846 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 911 911 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 925 925 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 968 968 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1013 1013 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1055 1055 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1086 1086 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1167 AA; 128983 MW; B8331C11SDCCCFD CRC64;

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Query Match 34.5%; Score 337; DB 1; Length 1167;

Best Local Similarity 37.2%; Pred. No. 9.8e-19; Matches 70; Conservative 46; Mismatches 70; Indels 2; Gaps 1;

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QY 3 QEDSDIAFLIDSGSIIIPDFRMRKEFVSTVMEQL--KSKTLFSLMQYSEEFRIHFTFK 60
Db 191 EDGTEIAIVLDGSGISGSDQKAKNFISTMRNRFYEKCFECNFPALVQYGAIVQTEFDLQ 250
QY 61 EFQNNPNRSLVLPITQLGRTHTATGIRKVRLEFNITNGARKNAKILVITDSEKFG 120
Db 251 ESRDINASLAKVQSIIVQYKEVTKTASAMQHLDNIFLPSRGRKKAUKWVVLTDGDI FG 310
QY 121 DPLGYEDVTPRADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 311 DPLMLTTVINSPKQGVVRFALGVGDPRFQNNNTYRELKLINSDPEAHTEFKVTNYSALDG 370
QY 181 IONQLREK 188
Db 371 LSLKLQQR 378

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Search completed: November 8., 2005, 21:26:17
Job time : 179 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2005, 21:12:18 ; Search time 42 Seconds
(without alignments)
339.476 Million cell updates/sec

Title: US-09-805-354-1

Perfect score: 976
Sequence: 1 CFQEDSDIAFLIDSGSIIP.....VNNFALKTIONQLREKXFA 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:.*
3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:.*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:.*
5: /cgn2_6/prodata/1/iaa/PCtUS_COMB.pep:.*
6: /cgn2_6/prodata/1/iaa/backfill.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	974	99.8	1152	2	US-08-476-062A-43
2	974	99.8	1152	5	PCT-US96-01314-43
3	974	99.8	1152	6	5424399-2
4	974	99.8	1152	6	5424399-2
5	974	99.8	1153	1	US-08-173-497-3
6	974	99.8	1153	1	US-08-286-889-3
7	974	99.8	1153	1	US-08-485-618-3
8	974	99.8	1153	1	US-08-362-652-3
9	974	99.8	1153	2	US-08-605-672-3
10	974	99.8	1153	2	US-08-482-293A-3
11	974	99.8	1153	2	US-08-943-363-3
12	974	99.8	1153	3	US-09-193-043-3
13	974	99.8	1153	4	US-09-688-307A-3
14	974	99.8	1153	4	US-09-350-259-3
15	960	98.4	187	2	US-08-177-109A-61
16	960	98.4	187	2	US-08-687-706-61
17	942	96.5	216	4	US-09-795-872-5
18	942	96.5	435	1	PCT-US95-04439-1
19	603	61.8	1151	1	US-08-286-889-37
20	603	61.8	1151	1	US-08-485-618-37
21	603	61.8	1151	1	US-08-362-652-37
22	603	61.8	1151	2	US-08-605-672-37
23	603	61.8	1151	2	US-08-482-293A-37
24	603	61.8	1151	2	US-08-943-363-37
25	603	61.8	1151	3	US-09-193-043-37
26	603	61.8	1151	4	US-09-688-307A-37
27	603	61.8	1151	4	US-09-350-259-37

ALIGNMENTS

28	603	61.8	1161	1	US-08-485-618-55	Sequence 55, Appl
29	603	61.8	1161	1	US-08-362-642-55	Sequence 55, Appl
30	603	61.8	1161	2	US-08-605-672-55	Sequence 55, Appl
31	603	61.8	1161	2	US-08-482-293A-55	Sequence 55, Appl
32	603	61.8	1161	3	US-09-943-363-55	Sequence 55, Appl
33	603	61.8	1161	3	US-09-193-043-55	Sequence 55, Appl
34	603	61.8	1161	4	US-09-688-307A-55	Sequence 55, Appl
35	603	61.8	1161	4	US-09-350-259-55	Sequence 55, Appl
36	602	61.7	413	1	US-08-485-618-101	Sequence 101, App
37	602	61.7	413	2	US-08-605-672-101	Sequence 101, App
38	602	61.7	413	2	US-08-482-293A-101	Sequence 101, App
39	602	61.7	413	2	US-08-943-363-101	Sequence 101, App
40	602	61.7	413	3	US-09-193-043-101	Sequence 101, App
41	602	61.7	413	4	US-09-688-307A-101	Sequence 101, App
42	602	61.7	413	4	US-09-350-259-101	Sequence 101, App
43	594	60.9	1155	1	US-08-286-889-46	Sequence 46, Appl
44	594	60.9	1155	1	US-08-485-618-46	Sequence 46, Appl
45	594	60.9	1155	1	US-08-362-652-46	Sequence 46, Appl

RESULT 1

US-08-476-062A-43

Sequence 43, Application US/08476062A

Patent No. 5877275

GENERAL INFORMATION:

APPLICANT: Arnaout, M. Amin

TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY

TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/476,062A

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/216,081

FILING DATE: 21-MAR-1994

APPLICATION NUMBER: 07/637,830

FILING DATE: 04-JAN-1991

APPLICATION NUMBER: 07/539,842

FILING DATE: 18-JUN-1990

APPLICATION NUMBER: 07/212,573

FILING DATE: 28-JUN-1988

ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 00786/068003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ. ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 1152 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-476-062A-43

Query Match 99.8%; Score 974; DB 2; Length 1152;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 60
DB 144 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IONOLREKIFA 191
DB 324 IONOLREKIFA 334

RESULT 2

PCT-US96-01314-43
Sequence 43, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSES: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1152
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US96-01314-43

Query Match 99.8%; Score 974; DB 2; Length 1152;

Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 60
DB 144 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120

DB 204 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IONOLREKIFA 191
DB 324 IONOLREKIFA 334

RESULT 3

5424399-2
Patent No. 5424399
APPLICANT: ARNAOUT, M. AMIN
TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/78,871
FILING DATE: 16-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 212,573
FILING DATE: 28-JUN-1988
SEQ ID NO: 2;
LENGTH: 1152
5424399-2

Query Match 99.8%; Score 974; DB 6; Length 1152;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 60
DB 144 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IONOLREKIFA 191
DB 324 IONOLREKIFA 334

RESULT 4

5424399-2
Patent No. 5424399
APPLICANT: ARNAOUT, M. AMIN
TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/78,871
FILING DATE: 16-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 212,573
FILING DATE: 28-JUN-1988
SEQ ID NO: 2;
LENGTH: 1152
5424399-2

Query Match 99.8%; Score 974; DB 6; Length 1152;

Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 60

DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNPRLSLVKEPIITQLGRTHTATGIRKRVRELFINITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNPRLSLVKEPIITQLGRTHTATGIRKRVRELFINITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IONQLREKXFA 191
DB 324 IONQLREKIFA 334

RESULT 5
US-08-173-497-3
Sequence 3, Application US/08173497

Patent No. 5437958

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

TITLE OF INVENTION: No. 5437958 Human 2 Integrin Alpha

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 S. Wacker Drive, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,497

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5437958and, Greca E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/31363

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1153 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-173-497-3

Query Match 99.8%; Score 974; DB 1; Length 1153;

Best Local Similarity 99.5%; Pred. No. 1,4e-96;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNPRLSLVKEPIITQLGRTHTATGIRKRVRELFINITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNPRLSLVKEPIITQLGRTHTATGIRKRVRELFINITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180

DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IONQLREKXFA 191
DB 324 IONQLREKIFA 334

RESULT 6
US-08-286-889-3

Sequence 3, Application US/08286889

Patent No. 5470953

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Mich

TITLE OF INVENTION: No. 5470953 Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,889

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: P38,659

REFERENCE/DOCKET NUMBER: 27866/32168

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1153 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-286-889-3

Query Match 99.8%; Score 974; DB 1; Length 1153;

Best Local Similarity 99.5%; Pred. No. 1,4e-96;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNPRLSLVKEPIITQLGRTHTATGIRKRVRELFINITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNPRLSLVKEPIITQLGRTHTATGIRKRVRELFINITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IONQLREKXFA 191
DB 324 IONQLREKIFA 334

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RESULT 7
US-08-485-618-3
; Sequence 3, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,618
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-618-3

Query Match          99.8%; Score 974; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQLKSKTLPSLMQYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQLKSKTLPSLMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPTTOLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPTTOLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IONOLREKIFA 191
DB 324 IONOLREKIFA 334
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RESULT 8

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US-08-362-652-3
; Sequence 3, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,652
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-362-652-3

Query Match          99.8%; Score 974; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQLKSKTLPSLMQYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQLKSKTLPSLMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPTTOLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPTTOLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IONOLREKIFA 191
DB 324 IONOLREKIFA 334
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RESULT 9
US-08-605-672-3
; Sequence 3, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-3

Query Match 99.8%; Score 974; DB 2; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDRRMKEPVSTVMEOLKSKTLPFLMOYSEEPFIHFTPK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDRRMKEPVSTVMEOLKSKTLPFLMOYSEEPFIHFTPK 203
QY 61 EFQNNPNSRLVKEITOLLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNSRLVKEITOLLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGVEDVPEADREGVIRYIVIGVDAFRSEKSRQELNTIASKPRDHVFQVNNFEALKT 180
DB 264 DPLGVEDVPEADREGVIRYIVIGVDAFRSEKSRQELNTIASKPRDHVFQVNNFEALKT 323
QY 181 IONOLREKIFA 191
DB 324 IONOLREKIFA 334

RESULT 10
US-08-482-293A-3
Sequence 3, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-3

Query Match 99.8%; Score 974; DB 2; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDRRMKEPVSTVMEOLKSKTLPFLMOYSEEPFIHFTPK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDRRMKEPVSTVMEOLKSKTLPFLMOYSEEPFIHFTPK 203
QY 61 EFQNNPNSRLVKEITOLLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNSRLVKEITOLLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGVEDVPEADREGVIRYIVIGVDAFRSEKSRQELNTIASKPRDHVFQVNNFEALKT 180
DB 264 DPLGVEDVPEADREGVIRYIVIGVDAFRSEKSRQELNTIASKPRDHVFQVNNFEALKT 323
QY 181 IONOLREKIFA 191
DB 324 IONOLREKIFA 334

RESULT 11
US-08-943-363-3
Sequence 3, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica

```
/ TITLE OF INVENTION: No. 5837478e1 Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,363
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1153 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-943-363-3

Query Match          99.8%; Score 974; DB 2; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFRMKKEFVSTVMEQLKSKTLPFLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDFRMKKEFVSTVMEQLKSKTLPFLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPTTOLLGRTHATGIRKRVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPTTOLLGRTHATGIRKRVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKROELNTISKPRDHVFOVNNFEAKT 180
DB 264 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKROELNTISKPRDHVFOVNNFEAKT 323
QY 181 IQNQLREKXFA 191
DB 324 IQNQLREKXFA 334

RESULT 12
US-09-193-043-3
/ Sequence 3, Application US/09193043
/ Patent No. 6251395
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vlieten, Monica
/ TITLE OF INVENTION: No. 625195e1 Human 2
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/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/193,043
/ CURRENT FILING DATE: 1998-11-16
/ EARLIER APPLICATION NUMBER: 08/173,497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286,889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362,652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943,363
/ EARLIER FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 3
/ LENGTH: 1153
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-193-043-3

Query Match          99.8%; Score 974; DB 3; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFRMKKEFVSTVMEQLKSKTLPFLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDFRMKKEFVSTVMEQLKSKTLPFLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPTTOLLGRTHATGIRKRVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPTTOLLGRTHATGIRKRVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKROELNTISKPRDHVFOVNNFEAKT 180
DB 264 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKROELNTISKPRDHVFOVNNFEAKT 323
QY 181 IQNQLREKXFA 191
DB 324 IQNQLREKXFA 334

RESULT 13
US-09-688-307A-3
/ Sequence 3, Application US/09688307A
/ Patent No. 6432404
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vlieten, Monica
/ TITLE OF INVENTION: No. 6432404e1 Human Beta-2
/ FILE REFERENCE: 27866/36646
/ CURRENT APPLICATION NUMBER: US/09/688,307A
/ CURRENT FILING DATE: 2000-10-13
/ PRIOR APPLICATION NUMBER: 09/193,043
/ PRIOR FILING DATE: 1998-11-16
/ PRIOR APPLICATION NUMBER: 08/605,672
/ PRIOR FILING DATE: 1996-02-22
/ PRIOR APPLICATION NUMBER: 08/173,497
/ PRIOR FILING DATE: 1993-12-23
/ PRIOR APPLICATION NUMBER: 08/286,889
/ PRIOR FILING DATE: 1994-08-05
/ PRIOR APPLICATION NUMBER: 08/362,652
/ PRIOR FILING DATE: 1994-12-21
/ PRIOR APPLICATION NUMBER: 08/943,363
/ PRIOR FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 3
/ LENGTH: 1153
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-688-307A-3

Query Match          99.8%; Score 974; DB 4; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
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Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTLPFSIMQYSEEFRIHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTLPFSIMQYSEEFRIHFTPK 203
QY 61 EFQNNPNPRSLVLPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNPRSLVLPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 323
QY 181 IONQLREKXFA 191
DB 324 IONQLREKXFA 334

RESULT 14
US-09-350-259-3
Sequence 3, Application US/09350259
Patent No. 6620915
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6620915el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
EARLIER FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1153
TYPE: PRT
ORGANISM: Homo sapiens
US-09-350-259-3

Query Match 99.8%; Score 974; DB 4; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTLPFSIMQYSEEFRIHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTLPFSIMQYSEEFRIHFTPK 203
QY 61 EFQNNPNPRSLVLPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNPRSLVLPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 323
QY 181 IONQLREKXFA 191
DB 324 IONQLREKXFA 334

RESULT 15
US-08-177-109A-61
Sequence 61, Application US/08177109A
Patent No. 5869615

GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Ogleby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/177,109A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MU 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-177-109A-61

Query Match 98.4%; Score 960; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 4.2e-96;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTLPFSIMQYSEEFRIHFTPK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTLPFSIMQYSEEFRIHFTPK 60
QY 61 EFQNNPNPRSLVLPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 61 EFQNNPNPRSLVLPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
QY 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180
DB 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180
QY 181 IONQLRE 187
DB 181 IONQLRE 187

Search completed: November 8, 2005, 21:27:05
Job time: 43 secs

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Db 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120
QY 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180
Db 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180
QY 181 IQNQLREKXFA 191
Db 181 IQNQLREKIFA 191

RESULT 2
US-09-758-493-1
; Sequence 1, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Armaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-493-1

Query Match 99.8%; Score 974; DB 11; Length 191;
Best Local Similarity 99.5%; Pred. No. 3.6e-95;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFFRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60
Db 1 CPQEDSDIAFLIDSGSIIIPHDFFRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120
Db 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120
QY 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180
Db 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180
QY 181 IQNQLREKXFA 191
Db 181 IQNQLREKIFA 191

RESULT 3
US-10-144-259-1
; Sequence 1, Application US/10144259
; Publication No. US20030109691A1
; GENERAL INFORMATION:
; APPLICANT: Armaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-1

Query Match 99.8%; Score 974; DB 14; Length 191;
Best Local Similarity 99.5%; Pred. No. 3.6e-95;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFFRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60
Db 1 CPQEDSDIAFLIDSGSIIIPHDFFRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120
Db 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120
QY 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180
Db 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180
QY 181 IQNQLREKXFA 191
Db 181 IQNQLREKIFA 191

RESULT 4
US-09-945-265-4
; Sequence 4, Application US/09945265
; Patent No. US20020123614A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimacka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: CBN-002CP
; CURRENT APPLICATION NUMBER: US/09/945,265
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-265-4

Query Match 99.8%; Score 974; DB 9; Length 1152;
Best Local Similarity 99.5%; Pred. No. 4.3e-94;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFFRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDSGSIIIPHDFFRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120
Db 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 263
QY 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180
Db 264 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
Db 324 IQNQLREKIFA 334

RESULT 5
US-11-000-473-43

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; Sequence 43, Application US/11000473
; Publication No. US20050227296A1
; GENERAL INFORMATION:
; APPLICANT: Amnaut, M. Armin
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS
; FILE REFERENCE: 00786-267002
; CURRENT APPLICATION NUMBER: US/11/000,473
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US/09/592,617
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 08/380,167
; PRIOR FILING DATE: 1999-01-30
; PRIOR APPLICATION NUMBER: US 08/216,081
; PRIOR FILING DATE: 1994-03-21
; PRIOR APPLICATION NUMBER: US 07/637,830
; PRIOR FILING DATE: 1991-01-04
; PRIOR APPLICATION NUMBER: US 07/539,842
; PRIOR FILING DATE: 1990-06-18
; PRIOR APPLICATION NUMBER: US 07/212,573
; PRIOR FILING DATE: 1988-06-28
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16 to -1
; US-11-000-473-43

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Query Match          99.8%; Score 974; DB 20; Length 1152;
Best Local Similarity 99.5%; Pred. No. 4.3e-94;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKSTLPSLMQYSEEFRIHFTFK 60
    |||
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKSTLPSLMQYSEEFRIHFTFK 203
    |||
QY 61 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
    |||
DB 204 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
    |||
QY 121 DPLGYEDVIPADREGVIRYVIGVDGAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
    |||
DB 264 DPLGYEDVIPADREGVIRYVIGVDGAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
    |||
QY 181 IQNQLREKKFA 191
    |||
DB 324 IQNQLREKKFA 334
    |||

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RESULT 6
US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. US20020062008A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: NO. US20020062008A1 Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-06-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03

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; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-350-259-3

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Query Match          99.8%; Score 974; DB 9; Length 1153;
Best Local Similarity 99.5%; Pred. No. 4.3e-94;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKSTLPSLMQYSEEFRIHFTFK 60
    |||
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKSTLPSLMQYSEEFRIHFTFK 203
    |||
QY 61 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
    |||
DB 204 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
    |||
QY 121 DPLGYEDVIPADREGVIRYVIGVDGAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
    |||
DB 264 DPLGYEDVIPADREGVIRYVIGVDGAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
    |||
QY 181 IQNQLREKKFA 191
    |||
DB 324 IQNQLREKKFA 334
    |||

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RESULT 7
US-09-902-481A-1

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; Sequence 1, Application US/09902481A
; Publication No. US2003005440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (17...)
; OTHER INFORMATION:
; US-09-902-481A-1

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Query Match          99.8%; Score 974; DB 10; Length 1153;
Best Local Similarity 99.5%; Pred. No. 4.3e-94;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKSTLPSLMQYSEEFRIHFTFK 60
    |||
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKSTLPSLMQYSEEFRIHFTFK 203
    |||
QY 61 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
    |||
DB 204 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
    |||
QY 121 DPLGYEDVIPADREGVIRYVIGVDGAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
    |||
DB 264 DPLGYEDVIPADREGVIRYVIGVDGAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
    |||
QY 181 IQNQLREKKFA 191
    |||

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;; PRIOR FILING DATE: 2000-10-17
;; NUMBER OF SEQ ID NOS: 57
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 37
;; LENGTH: 187
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-346-863-37

Query Match 97.1%; Score 948; DB 15; Length 187;
Best Local Similarity 99.5%; Pred. No. 2e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 DSDIAFLIDGSGSIIIPHDPRRKKEFVSTVMEQLKSKKTLFSLIMQYSEEFRIHFTFKEFON 64
DB 1 DSDIAFLIDGSGSIIIPHDPRRKKEFVSTVMEQLKSKKTLFSLIMQYSEEFRIHFTFKEFON 60
OY 65 NPNPSLVKPIITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NPNPSLVKPIITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120
OY 125 YEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONQ 184
DB 121 YEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONQ 180
OY 185 LREKKFA 191
DB 181 LREKIFA 187

RESULT 15

US-10-615-515-9
; Sequence 9, Application US/10615515
; Publication No. US20040132974A1
; GENERAL INFORMATION:
; APPLICANT: FAGAN, RICHARD, JOSEPH
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2004
; CURRENT APPLICATION NUMBER: US/10/615,515
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/GB02/00107
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: GB 0100750.9
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-615-515-9

Query Match 97.1%; Score 948; DB 16; Length 187;
Best Local Similarity 99.5%; Pred. No. 2e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 DSDIAFLIDGSGSIIIPHDPRRKKEFVSTVMEQLKSKKTLFSLIMQYSEEFRIHFTFKEFON 64
DB 1 DSDIAFLIDGSGSIIIPHDPRRKKEFVSTVMEQLKSKKTLFSLIMQYSEEFRIHFTFKEFON 60
OY 65 NPNPSLVKPIITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NPNPSLVKPIITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120
OY 125 YEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONQ 184
DB 121 YEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONQ 180
OY 185 LREKKFA 191
DB 181 LREKIFA 187